

PS Claim 2; Page 30-33; 68pp; Japanese.

XX The present sequence is a protein from Morning Glory, which has vacuolar
CC pH regulatory activities. The protein enables flower colour to be
CC controlled via regulation of the vacuolar pH, colours can range from blue
CC to red in colour spectrum. The protein is useful in controlling flower
CC colour to give new breeds of colourful plants for cut flowers,
CC particularly applicable in horticulture.

XX Sequence 542 AA;

Query Match 100.0%; Score 2768; DB 22; Length 542;
Best Local Similarity 100.0%; Pred. No. 4,8e-270;
Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MARGSLILONSDLTFTSDNASVSNMFLVALLCACYLGHLLLEENRWVESTALLIGLCTG 60
   |||||||
DB 1 MARGSLILONSDLTFTSDNASVSNMFLVALLCACYLGHLLLEENRWVESTALLIGLCTG 60
QY 61 TGVVILLLSGGKSSHLVSEDLFFIYLLPPIIFNAGFOVKKKOFVNMTIMLFGAIGT 120
   |||||||
DB 61 TGVVILLLSGGKSSHLVSEDLFFIYLLPPIIFNAGFOVKKKOFVNMTIMLFGAIGT 120
QY 121 LISCSTIISFGAVKIFKHLDIDFLDEGDIYLAIGAFATDVCCTLOVLSODETPLLYSIVF 180
   |||||||
DB 121 LISCSTIISFGAVKIFKHLDIDFLDEGDIYLAIGAFATDVCCTLOVLSODETPLLYSIVF 180
QY 181 GGVVNDATSVYFNAIOSFDMTSPDKTGLHFGIGNFYLFSSFTFLGIGLCAIYIK 240
   |||||||
DB 181 GGVVNDATSVYFNAIOSFDMTSPDKTGLHFGIGNFYLFSSFTFLGIGLCAIYIK 240
QY 241 KLYFGHSTDREYALMMLSYLYIMAEFLYSGILTFVFCGIWMSHYTHWNTSSRYT 300
   |||||||
DB 241 KLYFGHSTDREYALMMLSYLYIMAEFLYSGILTFVFCGIWMSHYTHWNTSSRYT 300
QY 301 TRHSFTLSFVAETFLFYVGMDALDIEKWKFNKSGISAVASSILVGLLVGRAAEVF 360
   |||||||
DB 301 TRHSFTLSFVAETFLFYVGMDALDIEKWKFNKSGISAVASSILVGLLVGRAAEVF 360
QY 361 PLSEFLSNLAKKNSDKISFRQOIIIMWAGLMRGAVSIALAYKFTTSGTSHENAMIT 420
   |||||||
DB 361 PLSEFLSNLAKKNSDKISFRQOIIIMWAGLMRGAVSIALAYKFTTSGTSHENAMIT 420
QY 421 SVTVVLFSTVYVGLMTKPLINLLPPHKOMPSGHSMTTSEPPSKHFTVPLDNDPDS 480
   |||||||
DB 421 SVTVVLFSTVYVGLMTKPLINLLPPHKOMPSGHSMTTSEPPSKHFTVPLDNDPDS 480
QY 481 ESDMTGPEVAPRTALRMLRTPHTVHRKYRKFDSEKRPVFGRGVFPVAGSPVEQS 540
   |||||||
DB 481 ESDMTGPEVAPRTALRMLRTPHTVHRKYRKFDSEKRPVFGRGVFPVAGSPVEQS 540
QY 541 PR 542
   ||
DB 541 PR 542

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RESULT 2
AAB12786
ID AAB12786 standard; Protein; 555 AA.

XX AAB12786;

XX 23-NOV-2000 (first entry)

XX At1p1ex gmelini Na+ and H+ antiporter protein.

XX At1p1ex gmelini; Na plus and H plus antiporter protein;

XX Na+ and H+ antiporter protein; transformed plant; high salt tolerance.

OS At1p1ex gmelini.

XX JP2000157287-A.

XX

PD 13-JUN-2000.

XX 16-SEP-1999; 99JP-0261606.

XX 24-SEP-1998; 98JP-0269504.

XX (SHOK-) SHOKUBUTSU KOGAKU KK.

XX WPI: 2000-468209/41.

DR N-PSDB: AAB72926.

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RESULT 3

ID AAB73253 standard; Protein; 553 AA.

XX AAB73253;

XX

Query Match 76.9%; Score 2127.5; DB 21; Length 555;
Best Local Similarity 76.6%; Pred. No. 1.8e-205;
Matches 418; Conservative 50; Mismatches 65; Indels 13; Gaps 3;

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QY 5 LSSLILON--SDLTFTSDNASVSNMFLVALLCACYLGHLLLEENRWVESTALLIGLCTG 62
   |||||
DB 5 LSSLILON--SDLTFTSDNASVSNMFLVALLCACYLGHLLLEENRWVESTALLIGLCTG 62
QY 63 VVILLISGGKSSHLVSEDLFFIYLLPPIIFNAGFOVKKKOFVNMTIMLFGAIGT 122
   |||||
DB 63 VVILLISGGKSSHLVSEDLFFIYLLPPIIFNAGFOVKKKOFVNMTIMLFGAIGT 122
QY 123 SCSTIISFGAVKIFKHLDIDFLDEGDIYLAIGAFATDVCCTLOVLSODETPLLYSIVFGE 182
   |||||
DB 123 SCSTIISFGAVKIFKHLDIDFLDEGDIYLAIGAFATDVCCTLOVLSODETPLLYSIVFGE 182
QY 183 GGVVNDATSVYFNAIOSFDMTSPDKTGLHFGIGNFYLFSSFTFLGIGLCAIYIK 242
   |||||
DB 183 GGVVNDATSVYFNAIOSFDMTSPDKTGLHFGIGNFYLFSSFTFLGIGLCAIYIK 242
QY 243 YFGHSTDREYALMMLSYLYIMAEFLYSGILTFVFCGIWMSHYTHWNTSSRYT 302
   |||||
DB 243 YFGHSTDREYALMMLSYLYIMAEFLYSGILTFVFCGIWMSHYTHWNTSSRYT 302
QY 303 HSFATLSFVAETFLFYVGMDALDIEKWKFNKSGISAVASSILVGLLVGRAAEVFPL 362
   |||||
DB 303 HSFATLSFVAETFLFYVGMDALDIEKWKFNKSGISAVASSILVGLLVGRAAEVFPL 362
QY 363 SFLSNLAKKNSDKISFRQOIIIMWAGLMRGAVSIALAYKFTTSGTSHENAMIT 422
   |||||
DB 363 SFLSNLAKKNSDKISFRQOIIIMWAGLMRGAVSIALAYKFTTSGTSHENAMIT 422
QY 423 VTTVVLFSTVYVGLMTKPLINLLPPHKOMPSGHSMTTSEPPSKHFTVPLDNDPDS 482
   |||||
DB 423 VTTVVLFSTVYVGLMTKPLINLLPPHKOMPSGHSMTTSEPPSKHFTVPLDNDPDS 482
QY 482 DVGNHEDTTEPRTIVRPSLRLNAPHTVHRKYRKFDSEKRPVFGRGVFPVAG 541
   |||||
DB 482 DVGNHEDTTEPRTIVRPSLRLNAPHTVHRKYRKFDSEKRPVFGRGVFPVAG 541
QY 542 SPVEQS 547
   |||||
DB 542 SPVEQS 547

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Df		14-MAY-2001 (first entry)	
Xx		Protein regulating the pH of vacuoles.	
De		Vacuole pH regulation; flower colour.	
Kw		Nierembergia hybrida.	
Xx		MO200114560-A1.	
Ox		01-MAR-2001.	
Pn		24-AUG-2000; 2000WO-JP05722.	
Pd		24-AUG-1999; 99JP-0236800.	
Pt		(SUNR) SUNTORY LTD.	
Pt		Iida S, Tanaka S, Inagaki Y;	
Dr		WPI: 2001-191648/19.	
Nr		N-PsDB: AAF75765.	
Pt		Morning glory-originated gene encoding a protein with pH regulation activity in vacuoles, useful in controlling flower color to give new breeds of colorful plants for cut flowers, particularly applicable in horticulture -	
Pt		Example 7: Page 50-52; 68pp; Japanese.	
Cc		The present sequence is a protein, which has vacuolar pH regulatory activities. The protein enables flower colour to be controlled via regulation of the vacuolar pH, colours can range from blue to red in colour spectrum. The protein is useful in controlling flower colour to give new breeds of colourful plants for cut flowers, particularly applicable in horticulture.	
Sq	Sequence	553 AA:	
	Query Match	76.8%; Score 2124.5; DB 22; Length 553;	
	Best Local Similarity	77.0%; Pred. No. 3.7e-205;	
	Matches	415; Conservative 51; Mismatches 66; Indels 7; Gaps	
Oy	1	MAFGLSL-LQNSDLFTSDHASVSMNLFVALLCACIVLGHLEENRWNESITALIIGL	59
Dd	1	MAFDGTLTGKKNMNTTSDHQSVSNLFVALICACIVIGHLEENRMNNESTITLVIGS	60
Oy	* 60	CGGVYVILLSGKSSHLVFSEDFEYILLPITIRAGQVKKQFFVFMTIMFGAIG	119
Dd	61	CGVTIILLISGKSNHILVFSEDFEYILLPITIRAGQVKKSFPMSTIMFGAVG	120
Oy	120	TISCISIFGAVKTEFKHLDIDLFEGVDLAIGATFAARDVCCTLOVSODEPLIYSYV	179
Dd	121	TLISTIIISAGALIGTFKKMDICHLETGDYLALGAIFAATDSVCTILOVEETPLYSLV	180
Oy	180	FEEGVVNDATSVYLENAIOSFDMTSFDPKIGLHAFTGNFLYLEPSTFLVGIGLCAYTI	239
Dd	181	FEEGVVNDATSVYLENAVNQFNDFLSHTSCAKQLQIGNFLYLEPASTFLVGVAAGLLSAFI	240
Oy	240	KLYLGRHSTDDEVALLMMMLSTYLMAELFLSLGIYVFCGYMSHTTWNNTESSRY	299
Dd	241	KLYLGRHSTDDEVAIMIMAYLSYMAELFLSLGIYVFCGYMSHTTWNNTESSRY	300
Oy	300	TTRHSFATLSFEAFEFILFYGMADLIDEKMKFVKNSOGLSYAVSSILVLIVGRAFY	359
Dd	301	TTKHNFATLSFEAEFLFIFYGMADLIDEKMKFVSDSPETSKVSSILGLVLVGRGFY	360
Oy	360	PFLSLSLNLAKKNSSDKISFRQOIITWMAGLRGAVSIALAYNKFTTSGTSHENAIMI	419
Dd	361	PFLSLSLNLTKKNPBDKISFNQOYITWAGLRGAVSIMALAYNQFTRGHTQLRANAIMI	420
Oy	420	TSTVVVLFSTYVVEGLMKPLINLLPHKOMPSCGHSSMTTPSSPKFTYVPLDNOPD	479

Dd 421 TESTITVVFSTIVFEGLMKPELLLLPSOKH-----IRMISSEPMTPKSFVIPLDSDTD 476

Qy 480 SESDMITGGEVARPALRLMTRPTTHVARWRKFEDDSFMREPFVGGRGFVPVAGSPVE 538
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Db 477 SEADL--GNHYVRPRLMLRLLSTPRSHYIYWRKIDNMRNVFGRGCFVPPVPSPE 533

RESULT 4
AAB73252
XX AAB73252 standard; Protein: 540 AA.
AC AAB73252;
XX
DT 14-MAY-2001 (first entry)
DE Protein regulating the pH of vacuoles.
KM Vacuole pH regulation; flower colour.
OS Petunia hybrida.
PN WO200114560-A1.
PD 01-MAR-2001.
PF 24-AUG-2000; 2000WO-JP05722.
PR 24-AUG-1999; 99JP-0236800.
PA (SUNR) SUNTORY LTD.
PI Iida S., Tanaka S., Inagaki Y;
DR MPI: 2001-191648/19.
XX N-PsDB; AAF75764.

PT Morning glory-originated gene encoding a protein with pH regulation
pr activity in vacuoles, useful in controlling flower color to give new
pt breeds of colorful plants for cut flowers, particularly applicable in
horticulture -

XX Example 7; Page 42-45; 68pp; Japanese.

CC The present sequence is a protein, which has vacuolar pH regulatory
CC activities. The protein enables flower colour to be controlled via
CC regulation of the vacuolar pH, colours can range from blue to red in
CC colour spectrum. The protein is useful in controlling flower colour to
CC give new breeds of colourful plants for cut flowers, particularly
CC applicable in horticulture.

SQ Sequence 540 AA;

Query Match 76.0%; Score 2103.5; Db 22; Length 540;
Best Local Similarity 76.4%; Pred. No. 4.7e+203;
Matches 412; Conservative 51; Mismatches 69; Indels 7; Gaps 3;

Qy 1 MAFFGSILLONDD-LFTSPHASVSNNLFVALCACIYGLHLEENRWNESITALIIGL 59
 ||::: | | | :||| | :||||:|||||:|||||:||||| | | |
Db 1 MAPFDGTILGNDRKLTSDHSOVSNLFVALCICAIYGHLEERKNWESITALVIGS 60

Qy 60 CTGVVILLSGKSSHLVSEDLEFIYLPRIIFNAGPOVKKOFPVNFMTIMFGAIG 119
 ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 61 CTGIYVILLGGKNSHIIVESEDLEFIYLPRIIFNAGPOVKKSPPRFNTIMFGALG 120

Qy 120 TITSCTSIISFGAVKTFKHLDIFDLDPGDVLGAIFAARDSCVTIOVLSODETPLLYSLY 179
 ||| | | | : | | : | | : | | | | | | | | | | | | | | | | | | | |
Db 121 TIISFIISLIGAIGIFKKMNISLEGDYLAIGAIFSADVCTLOVINODETPLYSLY 180

Qy 180 FEEGVVNDATSVYLFAAISFDMTSPDKFIGFHIGNFLYFLFSFTLGVGIGLCAYII 239
 ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 181 FEELGVVDATSVYLFRNALIONFDLSHDTCRKAMELVGNFYLFASSTALCVAAAGLLSATYII 240

Qy 240 KKLTYGRHSHTDEVALMMMLSYLIYMELFYLSGITLVFCGIYMSHYTHWNTESSRV 299

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Db 241 KKIYFRHSTDRVALIMIMAYISYMAELFYLSAILTYFFGSIYMSHTWHTNESSRV 300
QY 300 TPRHSATISFVAEPIFYMDALDIEKMKFVNKSGSLVAVSIIYGLVRAAFV 359
Db 301 TKHHTATISFAETFIYVGMADLIEKMFVSDSPSISVQVSSILGLVGRAAV 360
QY 360 FPLSPLSNLAKKNSDKISFRQOIIIMWAGLRGAVSIALAYNKFTTSGHTSLHENAII 419
Db 361 FPLSPLSNLTKRPEAKISFNQOVTIWMAGLRGAVSIALAYNKFTTSGHTSLHENAII 420
QY 420 TSTVYVLESTYVFGIMTPELINLLPDKOMPSSGHSSTTSEPSPKHFTVPLDNDPD 479
Db 421 TSTVYVLESTYVFGIMTPELINLLPDKOMPSSGHSSTTSEPSPKHFTVPLDNDPD 476
QY 480 SESDMITGEVAPRTALRMLRPTHTVHRVYRKFPDPSFMRPVFGRGFVPVAGSPVE 538
Db 477 SEADL--EKHVPRPHSLRMLSTPSHTVHYIYMKRFDNALMRPVFGRGFVPVAGSPPTD 533

RESULT 5
AAB1832
ID AAB1832 standard; Protein; 535 AA.
XX
AC AAB1832;
XX
DT 07-NOV-2000 (first entry)
XX
DE Rice Na+/H+ antiporter, OSMHX1.
XX
KW OSMHX1; Na+/H+ antiporter; sodium/proton antiporter; countertransporter;
KW active transport; rice; transgenic plant; salt-tolerance.
XX
OS Oryza sativa.
XX
PN WO200037644-A1.
XX
PD 29-JUN-2000.
XX
PF 22-DEC-1999; 99WO-JP07224.
XX
PR 22-DEC-1998; 98JP-0365604.
XX
PA (NORO ) JAPAN MIN AGRIC FORESTRY & FISHERIES.
XX
PI Fukuda A, Tanaka Y;
XX
DR WPI: 2000-442672/38.
DR N-PSDB: AAA61876.
XX
PT DNA encoding a sodium ion and proton counter-transporter protein of
PT rice origin for production of salt tolerant rice transformants -
XX
PS Claim 1a; Fig 1; 43pp; Japanese.
XX
CC This sequence represents a novel rice Na+/H+ antiporter
CC (countertransporter), OSMHX1. The invention relates to OSMHX1 and
CC nucleic acids which encode it; vectors, host cells and transgenic plants
CC containing OSMHX1 nucleic acids; recombinant expression of OSMHX1; and
CC antibodies which recognise OSMHX1. OSMHX1 nucleic acids are useful in the
CC production of salt tolerant transgenic plants.
XX
SQ Sequence 535 AA;

Query Match 74.3%; Score 2055.5; DB 21; Length 535;
Best Local Similarity 76.4%; Pred. No. 3.2e-198;
Matches 401; Conservative 49; Mismatches 66; Indels 9; Gaps 3;

QY 16 TSDHAGVSMNLFVALICGIVLGHLEENRWNESITALIIGCTGVYIILSGKSGSH 75
Db 16 TSDYASVAVSINLFVALICGIVLGHLEENRWNESITALIIGCTGVYIILMTGKSGSH 75
QY 76 LVFSEDLFFIYLLPILIFNAGFOVKKQOFVNFMTIMLFGAIGTLISCSISFGAVKIF 135

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Db 76 LVFSEDLFFIYLLPILIFNAGFOVKKQOFVNFMTITLFGAGVTMISFTTISIAIAIF 135
QY 136 KHLIDFLPDEDYDAICAFATSDVCTLOYLSODEPPLYSIYFEGGVNDATSVLFN 195
Db 136 SRMNGITLDVDFLAIGAFISADSVCTLOYLNODERPYSIYFEGGVNDATSVLFN 195
QY 196 AIOSEDMTSEPPKIGLHFTGNFLYFLSSTFLGVLGICLAYIILKLYFGHSTDRVAL 255
Db 196 ALQNFVDLVIDAAVYLVKFLNGFYLFLSSTFLGFAGLLSAYIILKLYIGHSTDRVAL 255
QY 256 MMLMSYSIYMAELFYLSGILTYFEGCIYMSHTWHTNESSRVTTRHSATISFAETP 315
Db 256 MMLMAYISYMAELFDLSGILTYFEGCIYMSHTWHTNESSRVTTRHATATISFAETP 315
QY 316 IELVGMADLIEKMKFVNKSGSLVAVSIIYGLVGRAAVFPPLSPLSNLAKKNSD 375
Db 316 IELVGMADLIEKMEFRASDRPKSIGISILGLVIGRAAFVPLSPLSNLTKKAPNE 375
QY 376 KISFRQOIIIMWAGLRGAVSIALAYNKFTTSGHTSLHENAIIITVYVLESTYVFG 435
Db 376 KITWRQOYIIMWAGLRGAVSIALAYNKFTTSGHTSLHENAIIITVYVLESTYVFG 435
QY 436 MTKPLINLLPDKOMPSSGHSSTTSEPSPKHFTVPLDNDPDSEDMITGEVAPRTA 495
Db 436 MTKPLIRLLP-----ASGHP--VTSEPPSPKSLHSPDLTSMGSDLESTT--NIVRPS 486
QY 496 LRLMLRPTHTVHRVYRKFPDPSFMRPVFGRGFVPVAGSPVEOS 540
Db 487 LRLMLTPTHTVHYIYMKRFDNALMRPVFGRGFVPVAGSPTEOS 531

RESULT 6
AA40901
ID AA40901 standard; Protein; 538 AA.
XX
AC AA40901;
XX
DT 18-JAN-2000 (first entry)
XX
DE Arabidopsis thaliana Na/H transporter AtNHX1.
XX
KW Sodium; proton; antiporter; transporter; salt tolerance; salt management;
KW transgenic plant; survival; soil; farming; accumulation; irrigation;
KW crop.
XX
OS Arabidopsis thaliana.
XX
PN WO9947679-A2.
XX
PD 23-SEP-1999.
XX
PF 18-MAR-1999; 99WO-CA00219.
XX
PR 18-MAR-1998; 98US-0078474.
XX
PR 15-JAN-1999; 99US-0116111.
XX
PA (BLUM/) BLUMWALD E.
PA (APSE/) APSE M.
PA (SNEDE/) SNEEDEN W.
PA (AHAR/) AHARON G.
XX
PI Blumwald E, Apse M, Snedden W, Aharon G;
XX
DR WPI: 1999-571840/48.
DR N-PSDB: AA222591.
XX
PT Nucleic acid molecules encoding sodium/proton transport polypeptides,
PT useful in genetic engineering salt tolerance in crop plants -
XX
PS Claim 36; Fig 1A; 93pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule encoding

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CC a plant Na/H antiport (PNHX) transporter polypeptide, or a fragment
 CC and capable of increasing salt tolerance in a cell. This sequence
 CC corresponds to the AtNHX1 transporter from Arabidopsis thaliana.
 CC The Na/H transporter polypeptides provide a means of intracellular
 CC salt management, particularly in plants. The sequences are useful for
 CC producing transgenic plants that are capable of surviving in soil with
 CC high salt levels that would normally inhibit growth of the crop species.
 CC This would be useful in farming land in areas that are generally
 CC considered unproductive through salt accumulation and poor irrigation,
 CC e.g. in India, Australia, and prairies in USA or Canada. Commercial
 CC crops, such as potatoes, tomatoes, brassica, cotton, sunflower,
 CC strawberries, spinach, lettuce, rice, soybean, corn, wheat, rye, barley,
 CC atriplex, sorghum, alfalfa, salicornia and others would benefit from
 CC increased salt tolerance.

XX Sequence 538 AA;

Query Match 73.7%; Score 2041; DB 20; Length 538;
 Best Local Similarity 73.8%; Pred. No. 9.3e-197;
 Matches 399; Conservative 57; Mismatches 71; Indels 14; Gaps 4;

QY 5 LSLILQN-SDLFSDHASVSNMLFVALLCACIYLGHLLEENRWVESITALLIGLCTGV 63
 DB 2 LDSLVSKLPSLSTSDHASVVALNLFVALLCACIYLGHLLEENRWVESITALLIGLCTGV 61

OY 64 VILLISGKSSHLVFSDEDFEYIYLPPIINAGQVKKQFVNFMTIMFGALITLS 123
 DB 62 TLLLSKSKSSHLVFSDEDFEYIYLPPIINAGQVKKQFVNFMTIMFGAAGTIS 121

OY 124 CSIIISFGAVKIFKHLIDIFLDFGDLAIGALFAATDSVCTLOVLSODETPLLYSVFE 183
 DB 122 CTIISLGTQGFKKIDIGTFDGLDGLAIGALFAATDSVCTLOVLSODETPLLYSVFE 181

OY 184 VVNDATSVVLENAIOSFDMTSFDPKIGLHFTGNFLYFLSFTFLGVGIGLCAYITKLY 243
 DB 182 VVNDATSVVLENAIOSFDTLHINHEAAPHLLGNFLYFLSFTFLGAAAGLISAVYIKLY 241

OY 244 FGRHSDREVALMMLMAYLSYIMAEFLYLSGILYVFCGIYVSHYTMHNWESSRITRH 303
 DB 242 FGRHSDREVALMMLMAYLSYIMAEFLYLSGILYVFCGIYVSHYTMHNWESSRITKH 301

OY 304 SFATISFVAETFFLYVGMDALDIEKMKFVKNSQGLSAVSSILVGLIVGRAFPVPLS 363
 DB 302 TFAISFLAETFFLYVGMDALDIDIKMSVSPTPSTIAVSSILMGIVMGAAFPVPLS 361

OY 364 FLSNLAKKNSDKISFRQOIIIMWAGLMGAVSIALATYKTTSGHTSLHENAIMITSTV 423
 DB 362 FLSNLAKKNSDKISFRQOIIIMWAGLMGAVSIALATYKTTSGHTSLHENAIMITSTI 421

OY 424 TVVLSTVVFGLMTKPLNLLPRHKOMPSGHSMTT---SPSSPKHTVPLLDNOPS 480
 DB 422 TVCLSTVVFGLMTKPLNLLPRHKOMPSGHSMTT---HONATSMLSDDNPKSHIPLDQ--DS 471

OY 481 ESDMITGPEVAPRTALRMLRTPTVHRKYRKFPDSEFMRPVFGRGFVPEVAGSPVDS 540
 DB 472 FLEPSSNHNVPRPDSIRGLTRPTVHYWYKQFPDSEFMRPVFGRGFVPEVAGSPTERN 531

OY 541 P 541
 DB 532 P 532

RESULT 7
 AAB73254
 ID AAB73254 standard; Protein: 555 AA.
 XX AAB73254;
 XX
 XX 14-MAY-2001 (first entry)
 XX
 DE Protein regulating the pH of vacuoles.
 XX
 XX Vacuole pH regulation; flower colour.

XX
 OS Torenia hybrida.
 XX
 PN WO200114560-A1.
 XX
 XX 01-MAR-2001.
 XX
 PF 24-AUG-2000; 2000WO-JP05722.
 XX
 XX 24-AUG-1999; 99JP-0236800.
 PR (SUNR) SUNTORX LMD.
 XX
 XX Iida S, Tanaka S, Inagaki Y;
 PI
 XX
 XX WPI: 2001-191648/19.
 DR N-PSDB; AAF75766.
 XX
 PT Morning glory-originated gene encoding a protein with pH regulation
 PT activity in vacuoles, useful in controlling flower color to give new
 PT breeds of colorful plants for cut flowers, particularly applicable in
 PT horticulture
 PS
 XX Example 7; Page 57-60; 68pp; Japanese.

CC The present sequence is a protein, which has vacuolar pH regulatory
 CC activities. The protein enables flower colour to be controlled via
 CC regulation of the vacuolar pH, colours can range from blue to red in
 CC colour spectrum. The protein is useful in controlling flower colour to
 CC give new breeds of colourful plants for cut flowers, particularly
 CC applicable in horticulture.

XX
 SQ Sequence 555 AA;

Query Match 70.6%; Score 1953.5; DB 22; Length 555;
 Best Local Similarity 70.5%; Pred. No. 6.4e-188;
 Matches 389; Conservative 56; Mismatches 88; Indels 19; Gaps 4;

OY 4 GLSLSL-----QNSDLTSDHASVSNMLFVALLCACIYLGHLLEENRWVESITALLIG 58
 DB 2 GFESVIRKLASETDNLMSSGHSVVAITLFTVLTCTIVGHLLEENRWVESITALLIG 61

OY 59 LCTGVILLISGKSSHLVFSDEDFEYIYLPPIINAGQVKKQFVNFMTIMFGAL 118
 DB 62 LATGVILLISGKSSHLVFSDEDFEYIYLPPIINAGQVKKQFVNFMTIMFGAV 121

OY 119 GTLISCSIIISFGAVKIFKHLIDIFLDFGDLAIGALFAATDSVCTLOVLSODETPLLYS 178
 DB 122 GTLISFIIISLGTIAFPKMMR-LGVGDYLAIGALFAATDSVCTLOVLSODETPLLYS 180

OY 179 VFGGVVNDATSVVLENAIOSFDMTSFDPKIGLHFTGNFLYFLSFTFLGVGIGLCAYI 238
 DB 181 VFGGVVNDATSVVLENAIÖSFDMTSFDPKIGLHFTGNFLYFLSFTFLGVGIGLSAYI 240

OY 239 IKKLYFGHSDREVALMMLMAYLSYIMAEFLYLSGILYVFCGIYVSHYTMHNWESSR 298
 DB 241 IKKLYFGHSDREVALMMLMAYLSYIMAEFLYLSGILYVFCGIYVSHYTMHNWENS 300

OY 299 VTRHSEFATLSFVAETFFLYVGMDALDIEKMKFVKNSQGLSAVSSILVGLIVGRAAF 358
 DB 301 VTRHSEFATLSFVAETFFLYVGMDALDIEKMKFVKNSQGLSAVSSILVGLIVGRAAF 360

OY 359 VEPFLSFLSNLAKKNSDKISFRQOIIIMWAGLMGAVSIALATYKTTSGHTSLHENA 418
 DB 361 VEPFLSFLSNLAKKNSDKISFRQOIIIMWAGLMGAVSIALATYKTTSGHTSLHENA 420

OY 419 ITSTVTVLVFSTVVFGLMTKPLNLLPRHKOMPSGHSMTTSPSSPKHTVPLLDNOP 478
 DB 421 ITSTITVLFSTVVFGLMTKPLNLLPRKLNRS-----VSSEPLRPNSITIPLLGESQ 475

OY 479 DSESMTT-----GEVAPRTALRMLRTPTVHRKYRKFPDSEFMRPVFGRGFV 530
 DB 476 DSVAFELFIRGOTSOGPEVAPRPSLRLTLTKPTVHYWYKRPDSEFMRPVFGRGFV 535

CC is a tonoplast pyrophosphatase hydrogen ion (H⁺) translocating pump.
 CC Transgenic plants can be made by transforming plant cells with exogenous
 CC tonoplast pyrophosphatase driven H⁺ pump genes and an exogenous nucleic
 CC acid encoding a protein, such as AVP1, which alters expression of
 CC vacuolar pyrophosphatase. Salt tolerance may be introduced into a plant
 CC via transformation of the cells to induce upregulation of vacuolar
 CC phosphatase expression. Drought and/or freeze tolerance may also be
 CC introduced through transformation with DNA encoding a vacuolar H⁺
 CC translocating pump linked to a promoter such as the 35S promoter. These
 CC processes are useful for bioremediating soil and removing cations such as
 CC sodium, calcium, manganese and lead from soil or water which can
 CC support plant growth. Plants which grow in saline soil can be produced
 CC and yield and flower size of plants can be increased.
 XX Sequence 571 AA;
 SQ
 Query Match 65.3%; Score 1808; DB 22; Length 571;
 Best Local Similarity 68.6%; Pred. No. 3.1e-173;
 Matches 371; Conservative 57; Mismatches 99; Indels 14; Gaps 4;
 QY 5 LSLILQN-SDLFTSDHASVSMNLFVALLCACIVLGHLEENRWNESTALITIGICGV 63
 DB 2 LDSLVSXKPLSLSTSDHASVVALNLPVALLCACIVLGHLEENRWNESTALITIGICGV 61
 QY 64 YILLISGKSSHLVSEDLFFIYLPPIIFNAGFOVKKOFVNFMTIMLFGAIGTLIS 123
 DB 62 TILLISGKSSHLVSEDLFFIYLPPIIFNAGFOVKKOFVNFMTIMLFGAIGTLIS 121
 QY 124 CSIIISFGAVKIFKHLDIDFDGDIYLAIGALFAATDSVCTIQVLSODETPILYSLVREG 183
 DB 122 CTIISLCVTOFPKKIDIGTFDLCYLAICAFPAATDSVCTIQVLSODETPILYSLVREG 181
 QY 184 VVNDATSVVLEFNATIOSFDMTSFDPKIGLHFGNLFYLFYSTPFGVIGILCAVITIKLY 243
 DB 182 VVNDATSVVLEFNATIOSFDMTSFDPKIGLHFGNLFYLFYSTPFGVIGILCAVITIKLY 241
 QY 244 FGRHSTDEVALMMMLSTYLIMAELEFYLSGILTFVFCGIYMSHYTHNVTSSRYTRH 303
 DB 242 FGRHSTDEVALMMMLSTYLIMAELEFYLSGILTFVFCGIYMSHYTHNVTSSRYTRH 301
 QY 304 SPATISPAETFEFLIYCOMDALDIEKKFVANSOGLSVANSSILVGLILVGRAAFVPLS 363
 DB 302 TFAATISPAETFEFLIYCOMDALDIEKKFVANSOGLSVANSSILVGLILVGRAAFVPLS 361
 QY 364 FLNLAKNNSDKISFROQIIMMAGLMRGAVSIALYKNTSTSGHSLHENAIMITSTV 423
 DB 362 FLNLAKNNSDKISFROQIIMMAGLMRGAVSIALYKNTSTSGHSLHENAIMITSTV 421
 QY 424 TVYLFSTVYVFGMLTKPLINLLPRHKQMPGSHSSMTT--SEPSPKHFTVPLDNOQPS 480
 DB 422 TVYLFSTVYVFGMLTKPLISYLLP-----HQNATTSMLSDDMTPKSHIHPLLDQ--DS 471
 QY 481 ESDMITGEVAPRALMLLTPTHTHYRWKRRKDDSFMRPVFEGRGFPVAVASPEVQS 540
 DB 472 FIEPSCHNHNPRPDSINGELFRTPTVHYRWKRRKDDSFMRPVFEGRGFPVAVASPEVQS 531
 QY 541 P 541
 DB 532 P 532
 RESULT 10
 AAY40902
 ID AAY40902 standard; Protein: 529 AA.
 XX AAY40902;
 XX
 DT 18-JAN-2000 (first entry)
 XX Arabidopsis thaliana Na/H transporter AtNHX2.
 DE
 XX Sodium; proton; antiport; transporter; salt tolerance; salt management;
 KM transgenic plant; survival; soil; farming; accumulation; irrigation;

KM crop.
 XX Arabidopsis thaliana.
 OS
 XX WO9947679-A2.
 PN
 XX 23-SEP-1999.
 PD
 XX
 PF 18-MAR-1999; 99NC-CA00219.
 XX
 PR 18-MAR-1998; 98US-0078474.
 PR 15-JAN-1999; 99US-0116111.
 XX
 PA (BLUM/) BLUMWALD E.
 PA (APSE/) APSE M.
 PA (SNEED/) SNEEDEN W.
 PA (AHAR/) AHARON G.
 XX
 PI Blumwald E, Apse M, Sneedden W, Aharon G;
 XX
 DR WPI, 1999-571840/48.
 DR N-P-SDB; AA222592.
 XX
 PT Nucleic acid molecules encoding sodium/proton transport polypeptides,
 PT useful in genetic engineering salt tolerance in crop plants -
 XX
 PS Claim 36; Fig 1B; 93pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule encoding
 CC a plant Na/H antiport (PNHX) transporter polypeptide, or a fragment
 CC and capable of increasing salt tolerance in a cell. This sequence
 CC corresponds to the AtNHX2 transporter from Arabidopsis thaliana.
 CC The Na/H transporter polypeptides provide a means of intracellular
 CC salt management, particularly in plants. The sequences are useful for
 CC producing transgenic plants that are capable of surviving in soil with
 CC high salt levels that would normally inhibit growth of the crop species.
 CC This would be useful in farming land in areas that are generally
 CC considered unproductive through salt accumulation and poor irrigation,
 CC e.g. in India, Australia, and prairies in USA or Canada. Commercial
 CC crops, such as potatoes, tomatoes, brassica, cotton, sunflower,
 CC strawberries, spinach, lettuce, rice, soybean, corn, wheat, rye, barley,
 CC atriplex, sorghum, alfalfa, salicornia and others would benefit from
 CC increased salt tolerance.
 CC
 SQ Sequence 529 AA;
 Query Match 57.8%; Score 1599.5; DB 20; Length 529;
 Best Local Similarity 58.7%; Pred. No. 2.9e-152;
 Matches 310; Conservative 87; Mismatches 120; Indels 11; Gaps 5;
 QY 1 MARGSSLLQNSDLFTSDHASVSMNLFVALLCACIVLGHLEENRWNESTALITIGIC 60
 DB 1 MARGSSLLQNSDLFTSDHASVSMNLFVALLCACIVLGHLEENRWNESTALITIGIC 58
 QY 61 TGVVILLISGKSSHLVSEDLFFIYLPPIIFNAGFOVKKOFVNFMTIMLFGAIGT 120
 DB 59 TGVVILLISGKSSHLVSEDLFFIYLPPIIFNAGFOVKKOFVNFMTIMLFGAIGT 118
 QY 121 LISCSIIISFGAVKIFKHLDIDFDGDIYLAIGALFAATDSVCTIQVLSODETPILYSLV 180
 DB 119 LISCSIIISFGAVKIFKHLDIDFDGDIYLAIGALFAATDSVCTIQVLSODETPILYSLV 178
 QY 181 GEGVNDATSVVLEFNATIOSFDMTSFDPKIGLHFGNLFYLFYSTPFGVIGILCAVITIK 240
 DB 179 GEGVNDATSVVLEFNATIOSFDMTSFDPKIGLHFGNLFYLFYSTPFGVIGILCAVITIK 238
 QY 241 KLYFGRHSTDEVALMMMLSTYLIMAELEFYLSGILTFVFCGIYMSHYTHNVTSSRYT 300
 DB 239 KLYFGRHSTDEVALMMMLSTYLIMAELEFYLSGILTFVFCGIYMSHYTHNVTSSRYT 298
 QY 301 TRHSFATLSFVAETFFIYVGMADLDIEKKFVANSOGLSVANSSILVGLILVGRAAFV 360
 DB 299 TRHSFATLSFVAETFFIYVGMADLDIEKKFVANSOGLSVANSSILVGLILVGRAAFV 358

Db 80 STLVTDPLIDSHAVEQEHNSLSLFEVICVIMGLILLIHSMLOTFQYLLPESIVVFLG 139

antibodies against the proteins, a method of identifying inhibitors of

CC the proteins, and compositions comprising the inhibitors for
 CC administration to an animal. The nucleic acids, and the proteins they
 CC encode may be used in the prevention, treatment and diagnosis of diseases
 CC associated with flea infestations. For example, the nucleic acids may be
 CC used to produce an HMT or HNC protein according to standard recombinant
 CC DNA methodology by inserting the nucleic acids into a host cell and
 CC culturing the cell to express the protein. The HMT and HNC nucleic acids
 CC may also be used as DNA probes in diagnostic assays (e.g., PCR) to detect
 CC and quantitate the presence of cat flea or other homologous nucleic acid
 CC sequences in samples. They may also be used to study the expression and
 CC function of the proteins and their role in metabolism. The HMT and HNC
 CC proteins may be used as antigens in the production of specific
 CC antibodies, and in assays to identify modulators (agonists and
 CC antagonists) of HMT and/or HNC protein expression and activity. The
 CC anti-HMT/HNC protein antibodies and antagonists may also be used to
 CC downregulate protein expression and activity. The antibodies may also be
 CC used as diagnostic agents for detecting the presence of flea polypeptides
 CC in samples (e.g., by enzyme linked immunosorbent assay (ELISA)). The
 CC present sequence represents a cat flea HMT protein of the invention.

XX Sequence 608 AA;

Query Match 21.58; Score 595; DB 21; Length 608;

Best Local Similarity 31.38; Pred. No. 6.6e-51;
 Matches 173; Conservative 114; Mismatches 190; Indels 76; Gaps 22;

QY 6 SSLQNSDLFTSDHASY-----VSMNLFVAL-LCAGTIVGHLLEEN--RWNESTALALI 56
 Db 59 NATIENPPVLPVEKGSMEQEOHSSMSIFVLCVLAALGILHFMQGFQFOLEPESIVVVF 118
 QY 57 IGLCTGVVILLSGKSSHL--VSEDELFYLLPPIIFNAGFOYKKOFVFNMTIM 113
 Db 119 LGALIGLILINIMSSKNILAMNKEAFSPFAFFVLLPPIIFESGYNLHKGFQNISIL 178
 QY 114 LEGAIGTILSISIFGAVKFKHLIDF-LDEGDYLAIGAFATPSVCTLOVL-SQDE 171
 Db 179 VFAIFGRIASFVVGAG-VYLGADVAAYNLSPVESFAFGSLISAVDPVAIVAFHADV 237
 QY 172 TPLLYSLVFEGGVNDATSVVLFNAIOSFD--MTSFDPKI-GLHFTGNFLYFLSSTFL 227
 Db 228 DPVLMVLVFGESILINDAISIYLTAVLESNNPMTTAEAVVSGIN---RCLMFAFAGI 294
 QY 228 GVGIGLCAYIIRKLYGRHSTDEVALMMLMSTLYSIMELEFYLSGILTFVFCGIYMSH 287
 Db 295 GVPFALISALILKHDVDRKKYPS-LELGMLVFTYAPVLAEGHLSGIMAILFCGIYMSH 353
 QY 288 YTMNHTVSSVTRHSPATLSFEVETFIPLYVGMDALDIEKMKFVANSQGLSVAVSSIL 347
 Db 354 YTHNLSIVJOITMOQTKRIATAETCVAFYLGMAIFSF-----RHREVPALVIMSVI 407
 QY 348 VGLILVGRAAVFPPLSELSNLAKKNSDKISFRQOIIIMWAGLARGAVSIALAVNKRFTTS 407
 Db 408 --LCLIGRAANIFPLSMVNLQFRHH--KITKKMAFIIMFSGL-RGAISVAL----- 453
 QY 408 GHTSLH-----ENAMITSTVTVVLFSTYVFGIMTKPKLINLLIPRHKQPSGHSSMTTS 461
 Db 454 ---LHMEFSDETHVHVIITLTLIVLCTTIFIGGATMPLKFL-----QANKKTSATRR 505
 QY 462 EPSSPKHFTVPL--ONOPSE--SDMITGPEVAPRTALBMLRTPTTHVHWRKRF-- 514
 Db 506 TRROOKAIIITLSKTRKMSAIDSELSELTTBEE-----RDVTFQVRRGLEEFIR 554
 QY 515 -DQSFMRPVRGGR 526
 Db 555 LDHRYLRPFRTRR 567

RESULT 13

ABB65651

ID ABB65651 standard; Protein; 727 AA.

XX AC ABB65651;

XX

DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 23745.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KM pharmacological.
 XX
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001: 2001MO-US09231.
 XX
 PR 23-MAR-2000: 2000US-191637P.
 XX
 PR 11-JUL-2000: 2000US-0614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX
 DR WPI: 2001-656860/75.
 DR N-PDB; ABL09754.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX
 PS Disclosure; SEQ ID NO 23745; 21bp + Sequence Listing; English.
 XX

CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABBS7737-ABBT2072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/publshd_pct_sequences.

XX Sequence 727 AA;

Query Match 20.8%; Score 575.5; DB 22; Length 727;

Best Local Similarity 28.8%; Pred. No. 7.9e-49;
 Matches 178; Conservative 99; Mismatches 196; Indels 145; Gaps 20;

QY 5 SSLQNSDLFTSDHASYVSMNLFVALLCAGTIVGHLLEEN--RWNESTALITIGLCTG 62
 Db 71 LNRIOISDLI-----VFVLLALVLTITLWFHHRHYSMLHETGLAVIIGLYVG 119
 QY 63 VILLISGKSSHL----- 77
 Db 120 AIIRY--AGTSATLVAMQVEPGVPTYSKLPDPDLMFRFPVNOQNGTRPREGITYAV 177
 QY 78 -----VSEDELFYLLPPIIFNAGFOYKKOFVFNMTTMLGAIGT 120
 Db 178 FRQGVHDVDEIDLKATQDPVEFNNILPPIIFAGYSLKRRKYFRNIGALITFAIVGT 237
 QY 121 LISCSITIS--FGAVKIF-KHLIDIDFLDGDYLAIGAFRAADSVCTLOVLSQDENPL-L 175
 Db 238 TLSAFILGGMFCVAKMLKMYLSSSR-TLDDSLYFGALISPDPLTILAIFNDLRVDVNL 296
 QY 176 YSLVGEGVNDATSVVLFNAIOS-----FDMTSFDPKIGLHFTGNFLYFLSST 225
 Db 297 YALVIGESVLDNAVAIVLGAIONGEHYSNTEFFETAF-----LRSLDPSFISLLSL 351
 QY 226 FLGVGIGLCAYIIRKLYGRHSTDEVALMMLMSTLYSIMELEFYLSGILTFVFCGIYM 285
 Db 352 MIGAANGCLTA-LMTKFTVRDPPLESALFVLMSTISFTFLAEATLGVAVAVFCGICQ 410

SQ Sequence 569 AA;

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0Y 24 SMNLFVALLCACVIEHL-----EENRWVNSIALIIGCTGCTVILLSSGKSSHL 76
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 34 SMAELILLV---LLIALLSTSYVSKIRRAIHETVSVYGVANVGLIIRVSPGLIQNM 90
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
0Y 77 LVFSEDLFFIYLLPPIIFNAGFOVRKKOFVNFMTIMFGAIGTLLISCSIIISFGA-VKIF 133
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 91 VSFHSTVFVFWLLPPIILNSGLEXHQSNEFNIGITILFPAAGTFTISA--VTLGVLYIE 144
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
0Y 136 KHLIDPLD--PEDYIAIAIRPADVSCITQVL-SODEPFLKSLVFEQGVVNAIV 193
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 149 SPLNENLMTFVEALSMKATLSAPDPTVALINSTRKVDOKLTYTIIFGSILINDVAIV 200
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
0Y 193 LFNAIOSFDMTSDPKIGIFH-----IGNFLYLFESTFELGVGIGLCAVYIIKKLYEGR 244
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 209 MEFTLQFGOKT-----LHFTLESGIGIFLIIFFLSILIGVSGIIGIALLAKTSYLRR 266
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
0Y 247 HSTREVALMMLMSYSLYIMAEFLISGLIVFPGIGVMHYTHMANTESSRYTTRHSPA 300
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 263 YPS-IESCIILAMATYFEFSGMCHSGVSLSCGTLLHAFENMSYKAKLSIKRYEPR 322
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
0Y 307 TLSFVAETFIFLVYGDAID-----IEKKFVNKSGSLVANSVSLIIGLIVGAAAFVPL 366
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 322 VLAQLSNFIFITIGMSLETFQVDVYKRPFIILIT---TVAVTA-----SKYMKVPL 378
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
0Y 363 SPLSLNAKK-----NSSDKISFROQIITIMWAGIMRGAVSIALYNNKFTTSGHSLHENA-I 411
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 371 SNLKNKFRBORNGLIDHIIPIYSOYMLTFWAGL-RGAVGVALA-----AGFES-ENQOT 422
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
0Y 418 MITSVNVYLESYVVGIMTKPILNL-----LPHKQMPs-----GHS 45
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 422 LRATLVVVVLTLLIFGGTARRLELTLITGVAAVDSDTEIGMLPMQOSPEDELENSA 48
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

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Oy  458 MTTSEPS-----SKR-----TVPILDNDPDESDMITGPEVAPRT-ALMLLRT 507
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  482 MELSDASAEPEVVVDQGFTEHDEGNTAPFLSKKVS-----TFEQYRAGAFNPFHS 536
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy  503 PRTVTHRYHRYMKRPDDSMRPV 522
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  537 SRDDQAMLTREDEVIKRV 556
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Search completed: October 18, 2002, 12:25:19
Job time : 38 secs

```

Search completed: October 18, 2002, 12:25:19
Job time : 38 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 18, 2002, 12:24:10 ; Search time 21 Seconds

(without alignments)
2480.020 Million cell updates/sec

Title: US-09-830-123-2

Perfect score: 2/68

Sequence: 1 MAFGLSLQNSLDLFTSPDA.....FGGRGFVPEVAGSEVQSPR 542

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 segs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR71:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	1732.5	62.6	457	2	Na+/H+-exchanging
2	591.5	21.4	703	2	hypothetical prote
3	568	20.5	633	2	hypothetical prote
4	556	20.1	569	2	probable sodium/hy
5	552.5	20.0	629	2	hypothetical prote
6	485.5	17.5	813	2	Na+/H+-exchanging
7	482.5	17.4	809	2	Na+/H+-exchanging
8	471.5	17.0	832	2	Na+/H+-exchanging
9	468.5	16.9	831	2	Na+/H+-exchanging
10	468	16.9	759	2	Na+/H+-exchanging
11	467.5	16.9	822	2	Na+/H+-exchanging
12	466	16.8	698	2	Na+/H+-exchanging
13	460.5	16.6	818	2	Na+/H+-exchanging
14	460	16.6	820	2	Na+/H+-exchanging
15	459.5	16.6	816	2	Na+/H+-exchanging
16	456.5	16.5	815	2	Na+/H+-exchanging
17	437.5	15.8	717	2	Na+/H+-exchanging
18	425.5	15.4	634	2	Na+/H+-exchanging
19	419	15.1	478	2	Na+/H+-exchanging
20	404	14.6	602	2	Na+/H+-exchanging
21	397.5	14.4	798	2	Na+/H+-exchanging
22	389.5	14.1	651	2	Na+/H+-exchanging
23	376	13.6	375	2	Na+/H+-exchanging
24	375	13.5	660	2	Na+/H+-exchanging
25	335.5	12.1	609	2	Na+/H+-exchanging
26	319	11.5	520	2	Na+/H+-exchanging
27	311.5	11.3	684	2	Na+/H+-exchanging
28	304	11.0	527	1	Na+/H+-exchanging
29	302	10.9	494	1	Na+/H+-exchanging

30	280.5	10.1	531	2	protein F20B17.4 (
31	275.5	10.0	528	2	probable Na+/H+ an
32	268	9.7	575	2	hypothetical prote
33	262.5	9.5	550	2	hypothetical prote
34	257.5	9.3	527	2	Na+/H+ antiporter
35	245.5	8.9	682	2	probable Na+/H+ an
36	243.5	8.8	682	2	probable Na+/H+ an
37	243	8.8	458	2	probable Na+/H+ an
38	243	8.8	517	2	Na+/H+ antiporter
39	235	8.5	490	2	Na+/H+ antiporter
40	234	8.5	565	2	sodium/proton exch
41	234	8.5	581	2	probable sodium/hy
42	226	8.2	650	2	probable Na+/H+ an
43	226	8.2	43	2	probable Na+/H+ an
44	226	8.2	680	2	conserved Na+/H+ an
45	224.5	8.1	540	1	Na+/H+-exchanging

ALIGNMENTS

RESULT 1

Na+/H+-exchanging protein 3 homolog A_TM021B04.4 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 22-Oct-1999

C:Accession: T01804

R:Dante, M.; Wamsley, P.; Gibson, A.

Submitted to the EMBL Data Library, June 1997

A:Description: The sequence of A. thaliana TM021B04.

A:Reference number: Z14440

A:Accession: T01804

A:Status: translated from GB/EMBL/DBD

A:Molecule type: DNA

A:Residues: 1-457 <DAN>

A:Cross-references: EMBL:AF007271; NID:92191181; PID:92191184; GSPDB:GN00063; ATSP-A

A:Experimental source: cultivar Columbia

C:Genetics:

A:Gene: ATSP-A_TM021B04.4

A:Map position: 5

A:Introns: 55/3; 95/2; 128/1; 148/1; 163/3; 240/3; 256/2; 286/3; 320/2; 400/3; 421/3

Query Match	Best Local Similarity	62.6%	Score 1732.5	ID 2	Length 457
Matches 341	Conservative 44	Mismatches 46	Indels 21	Gaps 3	
QY	5	LSLSLQN-SDLFSDHASVSMNLFVALLCACIVLGHLEENRWNESTALITGLCTGV	63		
DB	2	LDLSVSKLPSTSDHASVVALNLFVALLCACIVLGHLEENRWNESTALITGLCTGV	61		
QY	64	VILLSGKSSHLVFESEDLFFITLLPPIIFNMGFOVKKOPFNFTMLFGAIGLTIS	123		
DB	62	TILLISGKSSHLVFESEDLFFITLLPPIIFNMGFOVKKOPFNFTMLFGAIGLTIS	121		
QY	124	CSIIISFGAVKIFKHLIDFLFDGYLAIGALFATDSVCTLYLSODETPLYSLVFGEG	183		
DB	122	CTIISLQVQFFKKLDIGFDGLAIGALFATDSVCTLYLSODETPLYSLVFGEG	181		
QY	184	VVNATSVLVEFNATQSPDMSPDKIGLHFTGNFLYFLFSLTFLGCI	231		
DB	182	VVNATSVLVEFNATQSPDLTFLHNEAFHLLGNFLYFLFSLTFLGAVSPFLSSLPFLT	241		
QY	232	GLLCAYIIRKLKLYG-----RHSTDEVALIMLMSYLSYIAELFYLSGILTFPCGI	283		
DB	242	GLISAVYIKKLYGRMWHINCHRSIDREVALIMLMSYLSYIAELFDLSGILTFPCGI	301		
QY	284	VMSHYTHANVTESGRVTRHSFATLSFVAETFLYVGMADLDEKMKFYKNSGLSVAV	343		
DB	302	VMSHYTHANVTESGRITKHTFATLSFVAETFLYVGMADLDEKMKFYKNSGLSVAV	361		
QY	344	SSLVGLILVGRAVFPPLSLNKKNSDKISRRQIITWAGLMGAVSIALAAYK	403		
DB	362	SSLVGLVWVGRAVFPPLSLNKKNSDKINFRMOVIMWSGLMRGAVSMALAYK	421		

OY 404 FTSGHTSLHENAIMITSTVTVLFSTVVEGL 435
 Db 422 FTRAGHTDVRGNAMITSTVTVLCFSTVVRNL 453

RESULT 2

226529
 hypothetical protein Y18D10A.6 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T26529

R:Harita, B.

submitted to the EMBL Data Library, December 1998

A:Reference number: Z20226

A:Accession: T26529

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-703 <MIL>

A:Cross-references: EMBL:AL034393; PIDN:CAA22320.1; CESP:Y18D10A.6

A:Experimental source: EMBL: clone Y18D10A

C:Genetics:

A:Gene: CESP:Y18D10A.6

A:Introns: 23/3; 56/1; 103/2; 246/3; 352/3; 492/2; 578/3

Query Match 21.4%; Score 591.5; DB 2; Length 703;
 Best Local Similarity 34.8%; Pred. No. 6.8e-37;
 Matches 162; Conservative 78; Mismatches 181; Indels 45; Gaps 13;

OY 27 LEVALCACIVYGHLEENRWVESITALLIGLCTGVVILLSGKSSHLVFSDELFEI 86
 Db 138 LEVIMLATLVHMLVSKIHMMPELALVALGALIG-SILSYSRDMSEIEALSVDVFL 196
 OY 87 YLLPPIINAGQVKKQFFVNFMTIMFGAIGTISCSISFGAVKIFKHLDIF-LDF 145
 Db 197 YLLPPIIENAVNLKGYEFSNFPILTFALFTTISAMVIGAG-LYLLGALGILFEFTF 255
 OY 146 GYLIALGAFATDSVCTLOVLSODET-PLIYSLVFGEGVNDATSVLF-----NAIOS 199
 Db 256 FEGCFAPAMIASVDVPGTILAFQAKVESLILMLVFGESMLNDASIVLATALRHAPS 315
 OY 200 FDMTSFDPKIGLHTGNFLYLEFLSTPLGVLGIGLCAVITIKLYFGRHSTDEVALMML 259
 Db 316 FMSLASEITTSAFV-TFTEMEFFSACLGIGLISALLFKHVDI-RKTPSLFEFALLIF 373
 OY 260 SYLSYIMAEFLYGLITVFCGIVMSHYTHNNTDESSRVTRHSEALSPFAEFIFLY 319
 Db 374 SYTPGFAPALDLSGIMAILFCGISMSQPTRHNSPIAOITFRHRTISFVAETSTPAY 433
 OY 320 YQMDALDIEKMKFVNKSGLSVAVSSIL--VGLILVGRAAFVPLSFLSNLAKKNSDKI 377
 Db 434 IGMAFETIK-----LNFAPWLIFMSVYVLCILGRACNVPLATLVNCKRKV--QI 481
 OY 378 SFRQOIIIMWAGIMGAVSIALAYNKFTTSGHTSLHENAIMITSTVTVVLFSTVVEGLMT 437
 Db 482 SKMNOIIMFVS-MRGAVCFALVLYM----DLDEKKKSILITVILFLETTIFLGSA 535
 OY 438 KPLINL-----LPRHKOMPSGHSMTTSEPPSPKHF 469
 Db 536 LPFISFINRCYPNEROKRRRTPRNKESTGNSSALMSKTKQMSFF 581

RESULT 3

S69734
 hypothetical protein YDR456w - yeast (*Saccharomyces cerevisiae*)

C:Species: *Saccharomyces cerevisiae*

C:Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 23-Mar-2001

C:Accession: S69734

R:Dieckrich, F.S.

submitted to the EMBL Data Library, August 1995

A:Description: The sequence of *S. cerevisiae* lambda 3641 and cosmids 9461, 9831, and 941

A:Reference number: S69555

A:Accession: S69734

A:Molecule type: DNA
 A:Residues: 1-633 <DIE>
 A:Cross-references: EMBL:U33007; NID:g927685; PID:g927695; GSPDB:GN00004; MIPS:YDR456
 C:Genetics:
 A:Gene: MIPS:YDR456w
 A:Map position: 4R
 C:superfamily: hypothetical protein yvvp

Query Match 20.5%; Score 568; DB 2; Length 633;
 Best Local Similarity 27.2%; Pred. No. 3.6e-35;
 Matches 166; Conservative 117; Mismatches 203; Indels 124; Gaps 19;

OY 8 LLONSDLFTSDHASY-----VSNM-----LEVALCACIVYGHLEEN-RWV 48
 Db 30 LILSPDLPGSDDDPIADDPVDLNPVTEKMPSSMALFIMLLISALMSYVTLQKIRAV 89
 OY 49 NESITALLIGLCTGVVILLSGKSSHLVFSDELFEIYLLPPIINAGQVKKQFFV 108
 Db 90 HETVLSTFYGMVIGLILIRMSPGHYIODTVFNFSYFFNVLPLIINSGEINQVFFNN 149
 OY 109 FMTIMFGAIGTILSCSISFGAVKIFKHLDIFLD--FGDYLAIGAFATDSVCTLOV 166
 Db 150 MLSTILFAPDGTISAVVIGI-LIYITPLGESIDISFADAMSVGATLSATDPYIISI 208
 OY 167 LSODET-PLIYSLVFGEGVNDATSVLFNAIOSFDMTSFDPKIGLHTGNFLYLEFS 225
 Db 209 FNAKYVDPKITYIIFGSLNDALSIYMFETCQKFGQPATFSVVEGAGLFLMFSVSL 268
 OY 226 FLVGIGLCAVITIKLYFGRHSTDEVALMMLSTLYSMALFSLGILVYFCGIYM 285
 Db 269 LIGLIGLILVALLKHTHIRRY-POIESCLILIAEYSFFSGCMSIVSLFCGITL 327
 OY 286 SHYTHNNTDESSRVTRHSEALSPFAEFIFLYQMDALDIEKMKFVNKSGLSVAVSS 345
 Db 328 KHYAYMSKRSQTTIKYIQLARLSENFITYLGHLEFTELYY----KPLILIVA 383
 OY 346 ILVGLILVGRAAFVPLS-----FLSNLAKKNS--DKISFRQOIIIMWAGL 390.
 Db 384 I---SICVAMCAVFLSQFVNMYRKYITRMSGITGENISVPDEIPYNOQMRTFAGL 440
 OY 391 MRGAVSIALAYN-----KFTTSGHTSLHENAIMITSTVTVVLFSTVVEGLMT 444
 Db 441 -RGAVGVALALGIGEXKFT-----LLATVLYVVLVLTIFFGTTAGMLLEVLA 487
 OY 445 -----LPRHKOMPSGHSMTTSEPPSPKHFVPLDNDPSSDMI 485
 Db 488 IKTCGISSEDTSDERPIEAPRAINLNGSSIQTDLGPRSD-----NNSPDISIDOF 539
 OY 486 -----TGPEVAPRALMLLRTPHYV----HRYWK 513
 Db 540 AVSSNKMILPNNISYTGNTFGINETENTSPNPARSMDKRLRDLGITFNSDSOMFON 599
 OY 514 FDDSFMRPVF 523
 Db 600 FDEQVLKPVF 609

RESULT 4

T37706
 probable sodium/hydrogen exchanger - fission yeast (*Schizosaccharomyces pombe*)

C:Species: *Schizosaccharomyces pombe*

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000

C:Accession: T37706

R:Murphy, L.; Harita, D.; Wood, V.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, June 1997

A:Reference number: Z21738

A:Accession: T37706

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-569 <MR>

A:Cross-references: EMBL:Z97208; PIDN:CAB10103.1; GSPDB:GN00066; SPDB:SPAC15A10.06

A:Experimental source: strain 972h-; cosmid c15A10

C:Genetics:

A:Gene: SPDB:SPAC15A10.06
 A:Map position: 1
 A:Introns: 11/1: 116/3: 356/3
 C:Superfamily: hypothetical protein yvyp

Query Match 20.1%; Score 556; DB 2; Length 569;
 Best Local Similarity 28.9%; Pred. No. 2.5e-34;

Matches 162; Conservative 119; Mismatches 181; Indels 98; Gaps 23;

```

OY 24 SNMLFVALLCACIVLGHLE-----EENRWNESITALLIGLCGVILLISGKSSHL 76
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 34 SWALFILLV---LIGALLTSTYVOSKRIKRAIHETVIVFVGAVGGLIRYSPGLIIONM 90
OY 77 LVFSEDLFFIYLLPPIINAGFOVKKQFVNFMTIMLFGAIGLISCSISFGA-VKIF 135
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 91 VSFHSTYFENVLLPPIILNSGELHQSNFNRNIGIILFFAAGPITSA--VTLGLVYIF 148
OY 136 KHLIDFLD--FGDYLAIGALFPAATDSVCTLOVL-SQDEPLVSLVFGEGVNDATSVV 192
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 149 SFNLFSNMTFVEALSGATLSATDPVTVALFNSYKVDOKLYITIFGESILNDAYAV 208
OY 193 LFNAIOSFDMTSEDPKIGLHGF-----IGNFLYLFSLSTFLVGIGLCAIYIKKLYR 246
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 209 MERTIQFOGKT-----LHFFTLFSGIGITITFFISLLIGVSLGILLALLKYSYLRR 262
OY 247 HSTDREVALMMLMSYLSTYMALEFLYSGILTVFPGIYMSHYTHMNVESRVTTRHSEA 306
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 263 YPS-IESCIILMAYTSYFESNGCHMSGVSLFCGILTKHAFPMNSYKAKLSTKYFR 321
OY 307 TLSFAEFIFLYVGMOLD-----IEKKFVKNSOGLSVANSSILVGLILVGRAAFVPL 362
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 322 VLAQISENFIFILGLMSLEFQVDLVYKPIFILIT--TVAVTA-----SRVMNVEPL 370
OY 363 SFLSNLAK-----NSSDKISFRQOIIIMWAGLMRGAVSIALAYKKFTSGTSLHENA-I 417
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 371 SNLNLKFRQNGNLIIDHPIYSIQMLFWAGL-RGAVGVALA-----AGEEG--ENQOT 421
OY 418 MITSTVIVLFFSTVVFGLMTRPLINL-----LPPHKQMP-----GHSS 457
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 422 LRATLVVVVLTLLIFGGTARMEILHIERGVADVDSDEIQLMPQSGPEPDLNSA 481
OY 458 MTTSPS-----SPKIF-----IYPLLDNOPDSSDMITPEVARPP-ALRMLIRT 502
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 482 MELSDASAEVAVVDOQFTTEHFDGEGNIAPLTSKRVSS-----TPEQYORAGAENOFHS 536
OY 503 PTHVHYRWKRFDSFMRPV 522
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 537 SRDQAOQLTRFDEVIKPV 556

```

RESULT 5

hypothetical protein F57C7.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000

C:Accession: T22848

R:White, S.

submitted to the EMBL Data Library, February 1996

A:Reference number: 219625

A:Accession: T22848

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-629 <WILL>

A:Cross-references: EMBL:269646; PIDN:CAA93476.1; GSPDB:GN00028; CESP:F57C7.2

A:Experimental source: clone F57C7

C:Genetics:

A:Gene: CESP:F57C7.2

A:Map position: X

A:Introns: 33/3: 81/1: 119/2: 155/3: 207/2: 239/1: 274/2: 304/1: 354/1: 386/3: 421/3: 45

Query Match

20.0%; Score 552.5; DB 2; Length 629;

Best Local Similarity 35.1%; Pred. No. 3.3e-34;

Matches 158; Conservative 77; Mismatches 162; Indels 53; Gaps 16;

```

OY 78 VFSDELFYLLPPIINAGFOVKKQFVNFMTIMLFGAIGLISCSISFGA---VKI 134
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 157 VFSSEVFENMLPPIINAGYSILKRHRFRNIGISLAIYVIGTISG---FETGLMFPV 212
OY 135 FKHLIDFLDGDYLAIGALFPAATDSVCTLOVLSQDEPL-LVSLVFGEGVNDATSVV 193
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 213 FTSIFQNGYSFKELFFGALISATDPYITISVRNDMVEADLALLFGESALNDAYAV 272
OY 194 FNAIOSFDMTSEDPKIGLHGFN---FLYLFSLSTFLVGIGLCAIYIKKLYRHRST 249
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 273 SEVENESTSS--EATLQDFGSAIAGAFVFGSLGFMICMNAFLTKMILLSEHNL 330
OY 250 DREVALMMLMSYLSTYMALEFLYSGILTVFPGCIWMSHYTHMNVESRVTTRHSA 309
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 331 -LESSLFLSYISFLVAEVCGLIVSVLFCGIAQAHYNNLSDSOSNTHFPHMS 389
OY 310 FVAETFFLYVGMOLDIEKKFVKNSOGLSVANSSILVGLIV--GRAAFVPLSLN 367
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 390 FIMSFFICYIGSV-----FVTNNQKMS--FSPLFLSITISRALFVPLSLMLN 440
OY 368 LAKNNSDKISFRQOIIIMWAGLMRGAVSIALAYKKFTSGTSLHENAIMITSVTVVL 427
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 441 IRRR---PKIPKRYQHMILFAGL-RGAMAFALA-----GRMTSTENRQIMFATTAV 489
OY 428 FSTV-VFGLMTRPLINLPPH-KQMPSGHSMITSEPSPKIFVPLDNDPDSMDI 485
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 490 IYVLVAVGGLISWIDLIQKHGRDAIEGQRLSNSMSSP-----ADQHSDDL 538
OY 486 TGPEVARPTALRMLRTPTHVHYRWKRPD 515
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 539 ESVPTVMSPLNPMDKA---FLPRKMYHFD 565

```

RESULT 6

Na+/H+-exchanging protein NHE-2 - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 05-Nov-1999

C:Accession: A46748; A47449

R:Wang, Z.; Orłowski, J.; Shull, G.E.

J. Biol. Chem. 268, 11925-11928, 1993

A:title: Primary structure and functional expression of a novel gastrointestinal isoform

A:Reference number: A46748; M0ID:93280160

A:Accession: A46748

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-813 <MAN>

A:Cross-references: GB:L11236; NID:9205318; PIDN:AAA72350.1; PID:9205319

R:Collins, J.F.; Honda, T.; Knobel, S.; Bulus, N.M.; Conary, J.; Dubois, R.; Glushan,

Proc. Natl. Acad. Sci. U.S.A. 90, 3938-3942, 1993

A:title: Molecular cloning, sequencing, tissue distribution, and functional expression

A:Reference number: A47449; M0ID:93248205

A:Accession: A47449

A:Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 117-813 <COL>

A:Experimental source: intestine

A>Note: sequence inconsistent with the nucleotide translation

A>Note: sequence extracted from NCBI backbone (NCBIN:130778, NCBI:P130779)

Query Match 17.5%; Score 485.5; DB 2; Length 813;

Best Local Similarity 28.0%; Pred. No. 8.3e-29;

Matches 148; Conservative 86; Mismatches 215; Indels 79; Gaps 18;

```

OY 14 LFTSDHASY--VSMLFVALLCACIVLGHLEE-NRWNESITALLIGLCGVILLIS 69
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 71 VFPLDHPYQIIPPEIWLMLSLAKIGFHLVHKLPTIPEPSCILMVGILLGIF--- 127
OY 70 GGSNSHLVFSDELFYLLPPIINAGFOVKKQFVNFMTIMLFGAIGTL-----ISC 124
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 128 GVDEKSPPAKMTDVFLLPPIVLDAGYFMPPEFENLGIIFWYAVVGLMNSIGIL 187

```

[illegible]

RESULT 7
A66747
Na+/H+-exchanging protein NHE-2 - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 28-Feb-1997
C:Accession: A46747
R:Ste, C.M.; Levine, S.A.; Yun, C.H.; Montrose, M.H.; Little, P.J.; Pouyssegur, J.; Donck
J. Biol. Chem. 268, 11917-11924, 1993
A:Title: Cloning and expression of a rabbit cDNA encoding a serum-activated ethylisoprop
A:Reference number: A46747; MUID:93280159
A:Accession: A46747
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-809 <TSED>
A:Experimental source: ileal villus cells
A:Note: sequence extracted from NCBI backbone (NCBIN:133350, NCBIIP:133351)

Query Match	17.4%	Score 482.5;	DB 2;	Length 809;
Best Local Similarity	27.8%;	Pred. No. 1.4e-26;		
Matches 147;	Conservative 86;	Mismatches 216;	Indels 79;	Gaps 18;
OY	14	LFTSPDASV---VSAMNLEVALLCACIVGHLLEE-NRWVNNSITALLIGLCTGVILLLS	69	
Db	70	VFTLDYPRHQIREFETLLMILSLAKIGFHLXHKPTIVPESCLIMVGILLGLGITF---	126	
OY	70	GKSKSHLVSEDDLFYYLLRPPIFNAGFOYKKKOFEVNEMTLMFGAIGTL-----ISC	124	
Db	127	GVDEKSPRPMKTDFEFLLYLPRIYVDLAGCFMPTRFEENLTIEFYAVAVGTLMNSIGIV	186	
OY	125	SISKGAVIKRKHIDPLDFGDYLAIQAIFADPSVTGLQVLSQ-DETPLLISVPSEG	183	
Db	187	SLFGICGLEAGLSITLTL--QNLLFESLISADPAVLAVFENIHVEOYIIIVPEES	243	
OY	184	VNDATSVTVLENALDSF----DMTSFDPKIGHFIIGNLFLYFLSTFELGVGIGLCAVI	239	
Db	244	LINDAVTVVLINLRFSCQMKTIERIDVFAG---IANFVGIGIVGLIGIFLGIAATT	300	
OY	240	KKLIFGRHSSTOREVALMMMLSYLMAELPYLGSILTFVPGGIYMSHYTMHNATESRV	299	
Db	301	R---FTTHIRIVIEPLFVFLYSILXYTAEHMHLGSIAMITACAMTMNKVYEENVSOKSYT	357	
OY	300	TTRHSFALSVAEFTEFFIYGYMDALDI---KKMFYVNSOGLSAVVSIIYGLIIVGRA	356	
Db	358	TIKFYFMKLSSVSELLPIEWGVSTVGNKHHEMNAAEV-----CFTLAECILIRA	406	

[illegible]

```

result 8
A40205
Na+/H+-exchanging protein 3 - rabbit
N:Alternate names: Na+/H+ antiporter
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change 05-Nov-1999
C:Accession: A40205
R:Seq. C.M.: Brant, S.R., Walker, M.S., Pouyssegur, J., Donowitz, M.
J. Biol. Chem. 267, 9340-9346, 1992
A:Title: Cloning and sequencing of a rabbit cDNA encoding an intestinal and kidney-sp
A:Reference number: A40205; MUID:92250540
A:Accession: A40205
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-832 <TSE>
A:Cross-references: Gb:M87007; NID:g165548; PIDN:AAA31420.1; PID:g165549
C:Keywords: transmembrane protein

```

```

Query Match      17.0%; Score 471.5; DB 2; Length 832;
Best Local Similarity 28.5%; Pred. No. 9.8e-26;
Matches 148; Conservative 92; Mismatches 197; Indels 83; Gaps 19;

QY      22 VYSNMILFVALLCACIV-IGHLLEENRWNRNSETITALIGTGVVILLGSGKSHLVE- 79 .
      : : : : | | | | : : : : | | | | : : | | : : |
Db      56 IIALWVLAASLAKIVFHLSH--KATSVYPESLMLLVGLVIGVIL-----AADIASFT 108
      : : : : | | | | : : : : | | | | : : | | : : |
QY      80 -SEDFEYIYLLPPIIFNNGFOYKKKQFVNEMTIMLFGAIGTLLISCSIIISGAVKIF--- 135
      : : : : | | | | : : : : | | | | : : | | : : |
Db      109 LRPVTFEYFLLPPIVLDAGYEMPNRLFPFNSGLSILLVAVGVTWMAATGSLXGVFLSG 168
      : : : : | | | | : : : : | | | | : : | | : : |
QY      136 --KHLDDIFLDGDIALGATPAATDSCVTLQVLSQ-DEPILYSLVSGEVDNATSV 192
      : : : : | | | | : : : : | | | | : : | | : : |
Db      169 IMGEIKIGLDD--LTFGSLIAAVDPVAVLAVEEYHVNVEYLFIVGESLNDATV 225
      : : : : | | | | : : : : | | | | : : | | : : |
QY      193 LFNALISQFDMTSFDPKIGLHF--IGNFLYFLSSTFGVIGIGLCAVILIKLYGRHST 249
      : : : : | | | | : : : : | | | | : : | | : : |
Db      226 LYNVQSFPTLGGDKVTVGDCVKGIYSEFVYVSLGTLVGVAFPLSLVTR---FTKIVR 282
      : : : : | | | | : : : : | | | | : : | | : : |
QY      250 DREVALMLMISLYSIAMELFYLSGITVFECGIVMSHYTNWHTDESSRVTRHSFATLS 309
      : : : : | | | | : : : : | | | | : : | | : : |
Db      283 VLEPGFVFIIYSYLSITSEMLSSIIIAITFCIGICQCKYKAVANISEQATTVRYTKMILA 342
      : : : : | | | | : : : : | | | | : : | | : : |
QY      310 FVAEFPPILYVGMDDLIEKKFVKNSGSLVAVSSIIYGLILVG--RAAFVFLSEFLN 367
      : : : : | | | | : : : : | | | | : : | | : : |
Db      343 SGAETIIFELDISAVDPLIMTW-----NTAFVILITLLEVSFPAIGVLOTWILN 393
      : : : : | | | | : : : : | | | | : : | | : : |
QY      368 LAKKNSDOKISPRQOIIIMWAGIMRGAVSIALAY---NKFPTSGHSTLHENAIIWTSFV 423
      : : : : | | | | : : : : | | | | : : | | : : |
Db      394 KRRMVOLEIT---DOVMSYGL- RGAVAFALVALLDNGK-----VKKENLFEVSFTI 441
      : : : : | | | | : : : : | | | | : : | | : : |
QY      424 TVVLESTVFGIMTKPILINLLPPRKQMPSGHSSMTSPSPKFTVPLLDNDPDSQD 483
      : : : : | | | | : : : : | | | | : : | | : : |
Db      442 IYVFTVIRIPOGLTIPVQWL---KVKRSEHREKLEKLGRAFDHIL-----SAIE 491
      : : : : | | | | : : : : | | | | : : | | : : |
QY      484 MITGPEVAPPTLRLMLRPTHTVHRY---WRKDDDSFM 519
      : : : : | | | | : : : : | | | | : : | | : : |
Db      492 DISG-----OIGNHYLNRDKKANPDREFL 514

```


[illegible]

RESULT 14
A40204
Na+/H+-exchanging protein 1 - rat
N:Alternate names: Na+/H+ antiporter
C:Species: Rattus norvegicus (Norway rat)
C:Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change 28-Feb-1997
C:Accession: A40204
J:Oriowski, J.; Kandasamy, R.A.; Shull, G.E.
J. Biol. Chem. 267, 9331-9339, 1992
A:Title: Molecular cloning of putative members of the Na/H exchanger gene family. cDNA
rally related proteins.
A:Reference number: A40204; MUID:92250539
A:Accession: A40204
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-820 <ORL>
A:Cross-references: GB:M85299
C:Keywords: transmembrane protein

Query Match	16.6%	Score 460	DB 2:	Length 820
Best Local Similarity	28.5%	Pred. No. 7,1e-27		
Matches 139	Conservative 98	Mismatches 180	Indels 70	Gaps 19
QY 48	VNESITALIIGLCYGVILLSGSKSHLVFSEDFIYLPPIIFNMGFOVKKKQFV	107		
Db 133	VPESCLIVGLVNG--LIKVGEPFPL--QSDVFLEPLPIILDGICFLPLRQFTE	188		
QY 108	NEMTIMLFGAIGTLLSCSIIS--FGAVKIFPKHLDIFLPGDYLAIGATFATDSYCTLO	165		
Db 189	NLGTILFAVGVFLMNAFLGGLLVAICVGGQINNIGLDTLLFGSITISAVDPAYVLA	248		
QY 166	VLSODE--PLILSLYBEEGVNDATSVYLFNAIQSDMTSPDKIGLH--FTG--NFLYL	220		
Db 249	VFEIHHINELLHLPFESLINDAVTVLYHLEFEESAYEY--VGISDIFPLSLFVY	305		
QY 221	FLSTPLGVGIGLCAVITIKLVEGRHSRDREVALMMMSLYSIAMLEFYLSGILYVF	280		
Db 306	SLGVEFGVGVYGYAATSR--FTSHIRYIEPLEFVLVSYMAVLSAEFLHLSIGMALA	362		
QY 281	CGIIVSHYTHNNTVTESSRVYTRHSFATLSEVAFETFFLYVGMDALDIE--KMKFKNQ	337		
Db 363	SGVVMRYVEANISHKHTTIKYLEFKMKMSVSSTLIFLGVSTVAGSGQMNTYV----	418		
QY 338	GLSVAVSILVGLLVGRAAFVPLSFLSLANKNSDKISFRQOIIIMWAGIMGAVSI	397		
Db 419	-----ISTLL--PCLIRVLGVLTWFMFIN--KPRIVKLPDPDQIIAYGVL--RGALAF	467		
QY 398	ALAVANKFTTSGHSLHENAIMTSYTVVLFSTVVGMLTKPLINLLPPLHQMSPGSHS	457		
Db 468	SLGI--LLDKKHPMCD--LEFLAITVYLFETVYOGMTIRPLVLDLAKKRO-----	516		
QY 458	MTTSPSPKHTVPLLDNQPDSESDMIGPEVAPRTALRMILRPTTHVHYWR-----K	513		
Db 517	--ETKRINEIHTQFLDH-----LITGIE-----DICGIGHHHMKDKLNR	556		
QY 514	FDDSEMR 520			

[illegible]

```

Db 335 FLYGYMAYLSAELPHLSGIMALLASGVYMRPYVANISHKSHITIXYFLKMWSSVSEFLI 394
QY 317 FLYVGMADLIE---KMKFYKNSOGLSVAVSSILVGLIVGRAAFVPLSFLSLAKKNS 373
|::|: | | |::| |: | |::| |
Db 395 FIFLGVSFVAGSHHNMNTEV-----ISTLL-FCLTARVGLGLTWFIN--KFR 440
QY 374 SDKISFROOIIIMWAGIMRGAVSIALAYNKTTSQHTSLHENAIMITSTVTVLFSVVF 433
|::| | |::| | |::| |: | |: | |: | |: | |: | |: | |: | |: |
Db 441 IVKLPPKQFIATYGL-RGAIATSLGY--LLDKHFPMD--LPLTALITVIFFTVVO 495
QY 434 GIMTKPLINLLPPHKQWPSGSHSMTSEPSPKHFTVPLDNOQDSESDMITGPEVARP 493
|: |::| | | |::| |: | |: | |: | |: | |: | |: | |: |
Db 496 GMTIRPLVDLAVKKQ-----ETKRSINEIHTQFLDH-----LITGIE---- 535
QY 494 TALRMLRFTPHTVHRYR---KFDSEMR 520
|: |::| | | |::| |: | |: | |: | |: | |: | |: | |: |
Db 536 -----DICGHYGHNHMKDLNRFNKKYYK 559

```

Search completed: October 18, 2002, 12:25:49
 Job time : 26 secs

ET	103	123	POTHE
TRANSMEM	103	123	FOIE
TRANSMEM	103	123	FOIE

```

FT TRANSMEM 142 162 POTENTIAL.
FT TRANSMEM 179 199 POTENTIAL.
FT TRANSMEM 220 240 POTENTIAL.
FT TRANSMEM 246 266 POTENTIAL.
FT TRANSMEM 292 312 POTENTIAL.
FT TRANSMEM 340 360 POTENTIAL.
FT TRANSMEM 382 402 POTENTIAL.
FT TRANSMEM 404 424 POTENTIAL.
FT TRANSMEM 447 467 POTENTIAL.
FT TRANSMEM 483 503 POTENTIAL.
SQ SEQUENCE 669 AA; 74161 MW; F6416596229F2639 CRC64;

```

Query Match 20.9%; Score 578.5; DB 1; Length 669;
 Best Local Similarity 29.6%; Pred. No. 7.5e-30;
 Matches 165; Conservative 110; Mismatches 178; Indels 105; Gaps 19;

```

QY 10 QNSDLFTSDHSAVSMNLFVALLCAGIVGLLEEN--RWNESITALLIGLCTGVILL 67
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 62 QAEESHRODSANL--IFILLTLTLITLWLFKRRARFLHETGLAMIVGLVGLVLR 118
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 68 -----LSGKSHLVSEDEFFIYLLPRTIENAGFQVKKOPFVNMFT 111
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 119 GHHVSDVNNVTLSCEVSSPTLLVTPDEVEFNILPRTIFAGYSILKRHFERNLGS 178
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 112 IMFLGALIGLSCSIIS--FGAVKIFK--HLDIDFLDFGDIYALGAFATDSVCTIQ 165
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 179 ILATVFLGALISCFYIGSIMGCVTLMKVTGLADDF-FTDCLLFGAIVSATDPVTILA 237
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 166 VLSODETPL-LYSLVFGESVNDATSVILFNAI-----QSFDMTSPDKGLHFI 214
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 238 IFHELOVDVELYALLFGESEVLNDAVAIVLSSIVAYOPAGDNSHFDVTAMKRSIGI--- 294
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 215 GNFILFSLSTFGLVIGLCAIYIK--KLYGRHSTDBREVALMLMSLYMALELYL 272
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 295 --FLGTFSSFGMAGATGVTLVTKFKL---REPQLLETGLFLMSKSTLLLEANGF 349
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 273 SGILVFFCGIYVSHYTMHNTESRVTTRHSFATLSFAVETFIPLYGMALDIEKKKF 332
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 350 TGVAVVLFPGIQAHTYNNLSTESQHRKQLFELLNLAENFISYMGTLFTFQNHVF 409
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 333 VKNSGLSVAVSSILVG---LLVGRAAFVPLSPSLNAKNSDKISFRQIIIMAG 389
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 410 -----NPTFVGAFVAFILGRANAIYPLSLNLNGRS--KIGSNFOHMMMPAG 456
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 390 LMRGAVSIALAVNKKFTTSGLTSLHENAIMITSVTVVLFSTVFGIMTKPLINLLPPHK 449
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 457 L-RGAAAFALAIR-----DIAFYARQMFSTLLIVFTVAVFGGTTAMLSCLE---- 504
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 450 QMPSGHSMTSEPPSPKHFVPLLDNOPDSESDMITGPEVARPALRMLLRTPTHYVHR 509
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 505 -----HIRVGV-----DSQEHGLGVENERRTT-----KAESAMLF 536
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 510 YMRKEDSPMRPVFEGRG 527
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 537 MMYNFDHNYLKLPLTHSG 554
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

```

RESULT 2
 NAH2_YEAST STANDARD; PRT; 633 AA.

```

AC Q04121;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Mitochondrial sodium/hydrogen exchanger (Mitochondrial Na(+)/H(+)
  DE exchanger).
GN NAH2 OR NHX1 OR YDR456W OR D946L.40.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
  OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.

```

```

RA Dietrich F.S., Mulligan J., Allen E., Araujo R., Aviles E., Berno A.,
RA Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M.,
RA Hunicke-Smith S., Hyman R., Komp C., Lashkari D., Lew H., Lin D.,
RA Mosedale D., Nakahara K., Namath A., Oefner P., Oh C., Petel F.X.,
RA Roberts D., Schramm S., Schroeder M., Shogren T., Shroff N.,
RA Winant A., Yelton M., Botstein D., Davis R.W.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98175963; PubMed=9507001;
RA Numata M., Petrecca K., Lake N., Orlowski J.;
RT "Identification of a mitochondrial Na+/H+ exchanger.";
RL J. Biol. Chem. 273:6951-6959(1998).
CC -1- FUNCTION: ELECTRONEUTRAL EXCHANGE OF PROTONS FOR NA+ AND K+ ACROSS
  CC THE MITOCHONDRIAL INNER MEMBRANE. CONTRIBUTES TO ORGANELLAR VOLUME
  CC AND CALCIUM HOMEOSTASIS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial.
CC -1- SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
  CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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  CC or send an email to license@isb-sib.ch).
CC
CC EMBL: U33007; AAB64861.1; -.
DR SGD; S0002864; NHX1.
DR InterPro; IPR000676; Na_H_Exchngt.
DR Pfam; PF00999; Na_H_Exchanger; 1.
DR PRINTS; PR01084; NAH5XCHNGR.
KW Transmembrane; Sodium transport; Transport; Symport; Mitochondrion.
FT TRANSMEM 62 82 POTENTIAL.
FT TRANSMEM 86 106 POTENTIAL.
FT TRANSMEM 118 138 POTENTIAL.
FT TRANSMEM 154 174 POTENTIAL.
FT TRANSMEM 177 197 POTENTIAL.
FT TRANSMEM 218 238 POTENTIAL.
FT TRANSMEM 259 279 POTENTIAL.
FT TRANSMEM 307 327 POTENTIAL.
FT TRANSMEM 353 373 POTENTIAL.
FT TRANSMEM 377 397 POTENTIAL.
FT TRANSMEM 432 452 POTENTIAL.
FT TRANSMEM 458 478 POTENTIAL.
SQ SEQUENCE 633 AA; 70147 MW; 9B771ABDE41CEB0A CRC64;

```

Query Match 20.5%; Score 568; DB 1; Length 633;
 Best Local Similarity 27.2%; Pred. No. 3.3e-29;
 Matches 166; Conservative 117; Mismatches 203; Indels 124; Gaps 19;

```

QY 8 LLONSDLFTSDHSAV---VSMN-----LFWALLCAGIVLG--HLLEN-RWV 48
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 30 LLPSDPLPGSDPPIAGDPVDLNVTEDEMSWALFIMLLLLLSALMSYYLQKRIRAV 89
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 49 NESITALLIGLCTGVVILLSGKSSHLVPSDEDFIYLLPRTIENAGQVKKOPFVN 108
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 90 HEVLSIFVGYVIGLITRMSGHHYIODTVFNSSYFENVLLPRTIENAGVLEQVNEFN 149
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 109 FMTIMGALITLSCSIISGANKIRKHLIDPLD--FGDYALAGAFATDSVCTQV 166
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 150 MSLILIRAIPTGFTISAVVIGI-IIVTWFLGLEISIDTISFDANASVGTLSATDPVILL 208
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 167 LSOEET-PLIYSLVFGESVNDATSVVLFNAIOSFDTSPDKIGLHFIQNFYLFLEST 225
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 209 FNAKYKVPKLTITIFGESLNDALSIYMFECQKFRHQRPATFSSVFGAGLFLMTFSVSL 268
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 226 FLVGVIGLCAIYIKKLYFGHSHSTREVALMLMSYLSYMAELFYSLGTVFPGCIYM 265
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 269 LIGVLIGLIVALLKHHIRRY-PQIESCLITLIVAYSFEFNSCHMSGIVSLFCGITL 327
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 286 SHYTMHNTESRVTTRHSFATLSFVAETFIPLYVGDAIDIEKKRVKNSOGLSVAVSS 345
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

```

```

Db      328 KHYATAYMNSRSQITIKIFOLLARLSENFITYLGLIELETVEELVY----KPLLIITVAA 3633
QY      346 ILVGLIIVGRAAFVFPPLS-----FLSNLARKNSS--DKISFQOQIITIMAGL 3900
Db      384 I--SICARMCVAFEPPLSQFNMVIYKTIKMSGTIGENISYDPEIDIPYQMMTEFAGL 4400
QY      391 MRGAVSILAAVN-----KETSHTSLHENAIMTISVTVVLPSTVVEGLMTRPLINL- 4444
Db      441 -RGAVGVALALGIOGEKFT-----LTAFLVYVAVLVIIIFGTTGGMLEVLN 4870
QY      445 -----LPRHKOMPSGHSSMTTSEPSSPKHFTVPLDNCOPDESQMDI 4855
Db      488 IKTGCISEEDTSDDEFDIEAPRAIINLNGSSIQCDLGPYS-----NNSPDISIDQF 5399
QY      486 -----TGEVAPRALMLLPTPHYV-----HRMYRK 5133
Db      540 AVSSNKNLPNNISITTTGGNTFGCLNETENTSFPARSSMDKRNLDKLTGTLFNSDSQFON 5999
QY      514 FDDSEFMRPVF 523
Db      600 FDEQVLKEVF 609

```

RESULT 3	STANDARD;	PRT;	813 AA.
1AH2_RAT			
AC	P48763; 016434;		
DT	01-FEB-1996 (Rel. 33, Created)		
DT	01-FEB-1996 (Rel. 33, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Sodium/hydrogen exchanger 2 (Na(+)/H(+) exchanger 2) (NHE-2) (H7).		
GN	SLC9A2 OR NHE2.		
OS	Rattus norvegicus (Rat).		
OC	Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxId=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A. (LONG ISOFORM).		
RC	TISSUE=Stomach;		
RX	MEDLINE=93280160; PubMed=7685026;		
RT	Wang Z., Orlowski J., Shull G.E.;		
RT	"Primary structure and functional expression of a novel		
RT	gastrointestinal isoform of the rat Na/H exchanger.";		
RL	J. Biol. Chem. 268:11923-11928(1993).		
RN	[2]		
RP	SEQUENCE FROM N.A. (SHORT ISOFORM).		
RC	STRAIN=SPRAGUE-DAWLEY; TISSUE=Small Intestine;		
RX	MEDLINE=93248205; PubMed=7683411;		
RT	Collins J.F., Honda T., Knobel S., Bulus N.M., Conary J.,		
RT	Dubois R., Ghishan F.K.;		
RT	"Molecular cloning, sequencing, tissue distribution, and functional		
RT	expression of a Na+/H+ exchanger (NHE-2).";		
RL	Proc. Natl. Acad. Sci. U.S.A. 90:3938-3942(1993).		
RN	[3]		
RP	SEQUENCE FROM N.A. (SHORT ISOFORM).		
RC	TISSUE=Liver;		
RX	MEDLINE=96129297; PubMed=8595899;		
RT	Ghishan F.K., Knobel S.M., Summar M.;		
RT	"Molecular cloning, sequencing, chromosomal localization, and tissue		
RL	distribution of the human Na+/H+ exchanger (SLC9A2).";		
CC	Genomics 30:25-30(1995).		
CC	-1- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED		
CC	BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL		
CC	CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD		
CC	SODIUM ION CHEMICAL GRADIENT. SEEMS TO PLAY AN IMPORTANT ROLE IN		
CC	COLONIC SODIUM ABSORPTION.		
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.		
CC	-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM (SHOWN HERE) AND A		
CC	SHORT FORM. ARE PRODUCED BY ALTERNATIVE SPLICING.		
CC	-1- TISSUE SPECIFICITY: PREDOMINANTLY IN SMALL INTESTINE, COLON, AND		
CC	STOMACH, WITH MUCH LOWER LEVELS IN SKELETAL MUSCLE, KIDNEY, BRAIN		
CC	TESTIS, UTERUS, HEART, AND LUNG.		
CC	-1- PTM: PHOSPHORYLATED (POSSIBLE).		

```
CC -I SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.
CC -I CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC
CC DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.
CC -I CAUTION: REF.3 SEQUENCE WAS ORIGINALLY THOUGHT TO ORIGINATE FROM
CC HUMAN.
-----
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CC or send an email to license@isb-slb.ch).
-----
DR EMBL; L11236; AAA72350.1; -.
DR EMBL; L11004; AAA75406.1; -.
DR EMBL; S81591; AAB36180.1; -.
DR InterPro: IPR000676; Nah_Exchange.f.
DR Pfam: PF00999; Na_H_Exchange; 1.
DR PRINTS; PR01084; NAEHCXNGR.
KW Transmembrane; Glycoprotein; Sodium transport; Transport; Symport;
KM Multigene family; Phosphorylation; Alternative splicing.
FT DOMAIN 1 13
FT FT 14 34
FT FT 35 80
FT FT 81 101
FT DOMAIN 102 107
FT TRANSMEM 108 128
FT DOMAIN 129 139
FT TRANSMEM 140 160
FT FT 161 169
FT DOMAIN 170 190
FT TRANSMEM 191 209
FT FT 210 230
FT TRANSMEM 231 237
FT FT 238 258
FT DOMAIN 259 278
FT TRANSMEM 279 299
FT FT 300 308
FT TRANSMEM 309 329
FT FT 330 361
FT TRANSMEM 362 382
FT DOMAIN 383 392
FT TRANSMEM 393 413
FT DOMAIN 414 430
FT FT 431 451
FT TRANSMEM 452 459
FT DOMAIN 460 480
FT TRANSMEM 481 813
FT CARBOHD 351 351
FT VARSPIC 1 116
FT CONFLICT 504 504
FT CONFLICT 610 616
FT CONFLICT 742 742
FT CONFLICT 786 786
SQ SEQUENCE 813 AA; 91402 MW; 29127267D70B5845 CAC64;

Query Match 17.5%; Score 485.5; DB 1; Length 813;
Best Local Similarity 28.0%; Pred. No. 7.6e-24;
Matches 148; Conservative 86; Mismatches 215; Indels 79; Gaps 18;

OY 14 LETSHASY---VSNMNVALLCACTIVGHLLEF-NRWYNESITALLIGLCGVAYILLS 69
DB 71 VETLDYPHVQIDPEFTLLMLLASIAKIGHLYHKIPTVPSCELLIMWGLLGITF-- 127
OY 70 GKSSHLVFESEDFEFLPLPIFNAGFOYKKOFNFNMIMFGAIGTL-----ISC 124
DB 128 GVDKSPAMKTQDVFKLLPPIVLADAGTYNMPTRFFENLGIIFYAVGCLMANSIGCL 187
OY 125 SIISGAVKIKFKHDDIFDLBEDVDTATGAIIPANDSVCTLOYLSQ-DETPLLVSIVFEG 183
DB 188 SIIFGICQIEAGCISITLL--QNLFESLSIAVDPVAVLVAFENIHNEOLYLIVGES 244
```

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QY 184 VVNDATSVLFLNATIOSF----DMTSPDKIGLHFIQNFYLFSLSTFLGVGIGLLCAVYI 239
DB 245 LINDAVTVLVLYNLFKRSFCQMKTTIQTVDVFAG---IANFVVGIGCVLIGLGFIAAFTT 301
QY 240 KKLVEGRHSTDEVALMMLMSYLSYIMAEFLYLSGILVFPFGCIWMSHYTHWNTSSRV 299
DB 302 R---FTNINIVIEPLFVFLYSYLSITAEFHLSGIMATACAMTKMYEENVSQSKYT 358
QY 300 TTRHSFATLSVAETEFILYVGMALDIE---KKFVKNSQGLSVANSSILVGLIVGRA 356
DB 359 TIKYFMKMLSSVSETLIFIFMGVSTVCGKNHNMMAFV-----CFTLAFCLIMRA 407
QY 357 AFVPEPLSLNLAKKNSDKISFRQOITIMWALMGAVSIALAYNKFPTTSGTSLHENA 416
DB 408 LGVEVLIVINMFR---TIPLEFKDQFIITAYGGL-RCALICFALVF---LLPAVFPFRKK 459
QY 417 IMTSTVTVLFSVTVFGLMTRKPLINLLPPHKOMPSGHSMTSPSSPKHFTVPLDN 476
DB 460 LFTTAIVIVFETVYILGITIRPLVEFL---DYKRSNKKQOAVSEIHCRRF-----DH 510
QY 477 QPDSSEDMITGPEVAPRTALMLRLTPHTVHYRW---KFDSEFMR 520
DB 511 VKTGIEDVC-----GHMGHNFWDRKFKKFDKYL 540

```

```

RESULT 4
ID NAH2_RABIT STANDARD; PRT; 809 AA.
AC P50482;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Sodium/hydrogen exchanger 2 (Na(+)/H(+) exchanger 2) (NHE-2).
GN SLC9A2 OR NHE2.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NEW ZEALAND WHITE;
RX MEDLINE=93280159; PubMed=7685025;
RA Tse C.-M., Levine S.A., Yun C.H., Montrose M.H., Little P.J.,
RA Pouyssegur J., Donowitz M.;
RT "Cloning and expression of a rabbit cDNA encoding a serum-activated
RT ethylisopropylamide-resistant epithelial Na+/H+ exchanger isoform
RT (NHE-2).";
RL J. Biol. Chem. 268:11917-11924(1993).
CC -1- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED
CC BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL
CC CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD
CC SODIUM ION CHEMICAL GRADIENT. SEEMS TO PLAY AN IMPORTANT ROLE IN
CC COLONIC SODIUM ABSORPTION.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: HIGH LEVELS IN INTESTINE AND KIDNEY.
CC -1- PTM: PHOSPHORYLATED (POSSIBLE).
CC -1- SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.
CC -1- CATION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC
CC DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.
CC -----
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CC -----
DR EMBL: L13733; -; NOT_ANNOTATED_CDS.
DR InterPro: IPR000676; Nah_Exchange.
DR Pfam: PF00999; Nah_Exchange; 1.
DR PRINTS: PR01084; NAHEXCHNGR.
KW Transmembrane; Glycoprotein; Sodium transport; Transport; Symport;

```

```

KW Multigene family; Phosphorylation.
FT DOMAIN 1 16
FT TRANSMEM 17 37
FT TRANSMEM 38 79
FT TRANSMEM 80 100
FT TRANSMEM 101 106
FT TRANSMEM 107 127
FT TRANSMEM 128 138
FT TRANSMEM 139 159
FT TRANSMEM 160 168
FT TRANSMEM 169 189
FT TRANSMEM 190 208
FT TRANSMEM 209 229
FT TRANSMEM 230 236
FT TRANSMEM 237 257
FT TRANSMEM 258 277
FT TRANSMEM 278 298
FT TRANSMEM 299 307
FT TRANSMEM 308 328
FT TRANSMEM 329 360
FT TRANSMEM 361 381
FT TRANSMEM 382 391
FT TRANSMEM 392 412
FT TRANSMEM 413 429
FT TRANSMEM 430 450
FT TRANSMEM 451 458
FT TRANSMEM 459 479
FT TRANSMEM 480 809
FT DOMAIN 350 350
FT CARBOHYD
SQ SEQUENCE 809 AA; 90744 MW; DBD00B45443DB7A6 CRC64;

```

```

Query Match 17.4%; Score 482.5; DB 1; Length 809;
Best Local Similarity 27.8%; Pred. No. 1.2e-23;
Matches 147; Conservative 86; Mismatches 216; Indels 79; Gaps 18;

```

```

QY 14 LFTSDHASY--VSMNLEVALLCACIYGLHLEE-NRWNESITALLIGLCTGVVILLIS 69
DB 70 VFTLDYPHVOIPFEITLMLLASLAKIGFHLHKLPIIVPESCLLIMVGLIGLIIF-- 126
QY 70 GKKSHLVSEDLFFIYLLPFIIFNAGFOYKKOFQVNMFTMLRGAILTL-----ISC 124
DB 127 GVDKSPPAKTKVFFLYLLPPIVDAGYFMPRPFPENGLTFWAVYGLTMSNGICIV 186
QY 125 SIISFGAVKIFKHLIDIFDFGDIYLAIGALFAATDSCTLOYLSQ-DETPLLYSLVFGG 183
DB 187 SLICIGQIEAFGLSDITLL---QNLFGSLISAVDVAVLAVENHVMQGLIIVFGSS 243
QY 184 VVNDATSVLFLNATIOSF----DMTSPDKIGLHFIQNFYLFSLSTFLGVGIGLLCAVYI 239
DB 244 LINDAVTVLVLYNLFKRSFCQMKTTIQTVDVFAG---IANFVVGIGCVLIGLGFIAAFTT 300
QY 240 KKLVEGRHSTDEVALMMLMSYLSYIMAEFLYLSGILVFPFGCIWMSHYTHWNTSSRV 299
DB 301 R---FTNINIVIEPLFVFLYSYLSITAEFHLSGIMATACAMTKMYEENVSQSKYT 357
QY 300 TTRHSFATLSVAETEFILYVGMALDIE---KKFVKNSQGLSVANSSILVGLIVGRA 356
DB 358 TIKYFMKMLSSVSETLIFIFMGVSTVCGKNHNMMAFV-----CFTLAFCLIMRA 406
QY 357 AFVPEPLSLNLAKKNSDKISFRQOITIMWALMGAVSIALAYNKFPTTSGTSLHENA 416
DB 407 LGVEVLIVINMFR---TIPLEFKDQFIITAYGGL-RCALICFALVF---LLPAVFPFRKK 458
QY 417 IMTSTVTVLFSVTVFGLMTRKPLINLLPPHKOMPSGHSMTSPSSPKHFTVPLDN 476
DB 459 LFTTAIVIVFETVYILGITIRPLVEFL---DYKRSNKKQOAVSEIHCRRF-----DH 509
QY 477 QPDSSEDMITGPEVAPRTALMLRLTPHTVHYRW---KFDSEFMR 520
DB 510 VKTGIEDVC-----GHMGHNFWDRKFKKFDKYL 539

```

RESULT 5

NAH2_HUMAN STANDARD: PRT: 812 AA.

AC Q9UBX0: 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Sodium/hydrogen exchanger 2 (Na(+)/H(+) exchanger 2) (NHE-2).

GN SLC9A2 OR NHE2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Colon;

RX MEDLINE=99375108; PubMed=10444453;

RA Malakooti J., Dandekar R.Y., Schmidt L., Layden T.J., Dudeja P.K., Ramaswamy K.;

RT "Molecular cloning, tissue distribution, and functional expression of the human Na(+)/H(+) exchanger NHE2.";

RL Am. J. Physiol. 277:G383-G390(1999).

RN [2]

RP SEQUENCE FROM N.A.

RA Hou S., Wohlschlag P.;

RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD SODIUM ION CHEMICAL GRADIENT. SEEMS TO PLAY AN IMPORTANT ROLE IN COLONIC SODIUM ABSORPTION.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- TISSUE SPECIFICITY: EXPRESSED IN SKELETAL MUSCLE, COLON AND KIDNEY. LOWER LEVELS IN THE TESTIS, PROSTATE, OVARY, AND SMALL INTESTINE.

CC -1- PTM: PHOSPHORYLATED (POSSIBLE).

CC -1- STIMULABILITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.

CC -1- CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.

CC -----

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CC -----

DR EMBL: AF073299; AAD41635.1; -

DR EMBL: AC007239; AAF19248.1; -

DR MIM: 600530; -

DR InterPro: IPR000676; NaH_Exchng.

DR Pfam: PF00999; Na_H_Exchange; 1.

DR PRINTS: PR01084; NAHEXCHNGR.

KW Transmembrane; Glycoprotein; Sodium transport; Transport; Symport; Multi-pass family; Phosphorylation.

FT DOMAIN 1 13

FT DOMAIN 13 33

FT DOMAIN 33 34

FT DOMAIN 34 79

FT DOMAIN 79 80

FT DOMAIN 80 100

FT DOMAIN 100 106

FT TRANSSEM 107 127

FT TRANSSEM 128 138

FT TRANSSEM 139 159

FT TRANSSEM 160 168

FT TRANSSEM 169 189

FT TRANSSEM 190 208

FT TRANSSEM 209 229

FT TRANSSEM 230 236

FT TRANSSEM 237 257

FT TRANSSEM 258 277

FT TRANSSEM 278 298

FT TRANSSEM 299 307

FT TRANSSEM 308 328

FT DOMAIN 329 360 EXTRACELLULAR (POTENTIAL).

FT TRANSSEM 361 381

FT TRANSSEM 382 391

FT TRANSSEM 392 412

FT TRANSSEM 413 429

FT TRANSSEM 430 450

FT TRANSSEM 451 458

FT TRANSSEM 459 479

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CC CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD
CC SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL
CC TRANSDUCTION.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- PPM: PHOSPHORYLATED (POSSIBLE).
CC -1- SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.
CC -1- CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC
CC DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.
CC -1- CAUTION: HYDROPHOBIC DOMAINS A, B AND L ARE NOT BELIEVED TO BE
CC TRANSMEMBRANAL, BUT ONLY MEMBRANE-ASSOCIATED.
CC -----
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CC -----
CC EMBL: U51112; AAA92976.1; -.
CC MGI: MGI:102462; Slc9a1.
CC InterPro: IPR000676; NaH_Exchange.
CC Pfam: PF00999; Na_H_Exchange; 1.
CC PRINTS: PR01084; NAHEXCHNGR.
CC Transmembrane; Glycoprotein; Sodium transport; Transport; Symport;
CC Multigene family; Phosphorylation.
CC DOMAIN 1 12 CYTOPLASMIC (POTENTIAL).
CC 1 13 A (M1) HYDROPHOBIC.
CC 2 32 CYTOPLASMIC (POTENTIAL).
CC 3 33 B (M2) HYDROPHOBIC.
CC 4 106 127 CYTOPLASMIC (POTENTIAL).
CC 5 128 130 CYTOPLASMIC (POTENTIAL).
CC 6 131 150 C (M3) (POTENTIAL).
CC 7 151 162 EXTRACELLULAR (POTENTIAL).
CC 8 163 183 D (M4) (POTENTIAL).
CC 9 184 188 CYTOPLASMIC (POTENTIAL).
CC 10 189 210 E (M5) (POTENTIAL).
CC 11 210 230 EXTRACELLULAR (POTENTIAL).
CC 12 231 251 F (M5A) (POTENTIAL).
CC 13 252 260 CYTOPLASMIC (POTENTIAL).
CC 14 261 282 G (M5B) (POTENTIAL).
CC 15 283 301 EXTRACELLULAR (POTENTIAL).
CC 16 302 322 H (M6) (POTENTIAL).
CC 17 323 336 CYTOPLASMIC (POTENTIAL).
CC 18 337 357 I (M7) (POTENTIAL).
CC 19 358 388 EXTRACELLULAR (POTENTIAL).
CC 20 389 410 J (M8) (POTENTIAL).
CC 21 411 416 CYTOPLASMIC (POTENTIAL).
CC 22 417 438 K (M9) (POTENTIAL).
CC 23 439 452 EXTRACELLULAR (POTENTIAL).
CC 24 453 473 L, HYDROPHOBIC.
CC 25 474 482 EXTRACELLULAR (POTENTIAL).
CC 26 483 503 M (M10) (POTENTIAL).
CC 27 504 820 CYTOPLASMIC (POTENTIAL).
CC 28 820 820 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC 29 374 374 CARBOHYD
CC 30 SEQUENCE 820 AA; 91467 MW; 0589C4D08D348BE CRC64;
CC -----
CC Query Match 17.1%; Score 472.5; DB 1; Length 820;
CC Best Local Similarity 28.4%; Pred. No. 5.2e-23;
CC Matches 145; Conservative 106; Mismatches 189; Indels 71; Gaps 21;
CC -----
CC 25 MNLFVALLACIVLGHLEEE-NRWYNESTITLIIIGCTGVVILLISGKSSHLVSEDL 83
CC :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
CC 109 ISMILILACIMKIGFHVPIPTISIVPESCLLVGLVGG-LIKGVGTPEFL--QSDV 164
CC :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
CC 84 FFLYLLPPIIFNAGFVKKKQFFVNMPTLMFGAIGTLISCTIS--FGAKVIFKHLDID 141
CC :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
CC 165 FFLFLPLPIIDAGYFLPRPTENIGTLIFAVVGTIMNAFPLGLGLYAVCLVGEQGIN 224
CC :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
CC 142 PLDFGFLYLGAFATSDVCTLOVLSODE-PLLYSYLVFEGGVNDAVTFNAIOSF 200
CC :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
CC 225 NIGLDLTLFGSLISAVDVAVLANVPEEIHNEHLIIVFGSLNDAVTVYLHLEEF 284
CC :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
CC 201 DMTSEDPKIGLH-FLG--NFLYFLSLSTFLGVGIGLCAVYIKKLYFGRHSTDEVALM 256
CC :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

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CC Db 285 --ASVD-SVGISDIFGLFSFVVALGVGVGVVIAFTSR--FTSHRVIEPLEV 338
CC :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
CC QY 257 MMSYSLYIAELFYLSGILTFVFCGIWMSHYMHVWYESSRNTFRHSATLSFAAEFI 316
CC :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
CC Db 339 FLVSYMYLAEFLHJSLGIMALLASGVMPKPYEAMISHTTLYFLKMSVSESLI 398
CC :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
CC QY 317 FLVYGMADLIE---KWKFEYKNSQGLSAVSSILVGLIIVGRAAEVPLSPLSNLAKNS 373
CC :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
CC Db 399 FFLGVSTVAGSHQWMTVF-----ISTLL--FCLLARTGLVLTWFLIN--KFR 444
CC :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
CC QY 374 SDRISFRQOIIIMWAGLMRGAVSIALVYKFTTSGHTSLHENAIMTSVTVLVSTVF 433
CC :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
CC Db 445 IVKLTMPDQFLIAYGVL-RGAIAFSLGY--LIDKHKFPMCD--LFLTALITYVFFVFO 499
CC :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
CC QY 434 GLMKPLINLLLPPIHQMPSGSHSMTSPSPKHTFPLLDNQPDSESDMITGPVAVP 493
CC :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
CC Db 500 GMTIRPLVDLVAVKKQ-----ETKRSINEIHTQFLDH-----LITGIE--- 539
CC :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
CC QY 494 TALMLLRPTHTVHYRYWR---KFDSEFWR 520
CC :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
CC Db 540 -----DTCGHYGHNMKDKLRFKRYK 563
CC :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
CC -----
CC RESULT 7
CC NAH3_RABIT STANDARD; PRT: 832 AA.
CC ID NAH3_RABIT
CC AC P26432;
CC DT 01-AUG-1992 (Rel. 23, Created)
CC DT 01-AUG-1992 (Rel. 23, Last sequence update)
CC DT 15-JUL-1999 (Rel. 38, Last annotation update)
CC DE Sodium/hydrogen exchanger 3 (Na(+)/H(+) exchanger 3) (NHE-3).
CC GN SLC9A3 OR NHE3.
CC OS Oryctolagus cuniculus (Rabbit).
CC OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
CC OX NCBI_TaxId=9986;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=NEW ZEALAND WHITE; TISSUE=ileal villus, and kidney cortex;
CC RX MEDLINE=92250540; PubMed=1374392;
CC RA Tse C.-M., Brant S.R., Walker S.S., Pouyssegur J., Donowitz M.;
CC RT Cloning and sequencing of a rabbit cDNA encoding an intestinal and
CC RT kidney-specific Na+/H+ exchanger isoform (NHE-3).";
CC RL J. Biol. Chem. 267:9340-9346(1992).
CC CC -1- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED
CC BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL
CC CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD
CC SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL
CC TRANSDUCTION.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: INTESTINAL AND KIDNEY SPECIFIC. MOST ABUNDANT
CC IN KIDNEY CORTEX, FOLLOWED EQUALLY BY ILEUM AND ASCENDING COLON,
CC THEN KIDNEY MEDULLA AND JEJUNUM. IS ABSENT FROM DUODENUM AND
CC DESCENDING COLON.
CC -1- PPM: PHOSPHORYLATED (POSSIBLE).
CC -1- SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.
CC -1- CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC
CC DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.
CC -----
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CC -----
CC EMBL: M87007; AAA31420.1; -.
CC PIR: A40205; A40205.
CC DR InterPro: IPR000676; NaH_Exchange.
CC DR Pfam: PF00999; Na_H_Exchange; 1.
CC DR PRINTS: PR01084; NAHEXCHNGR.

```

KW Transmembrane; Glycoprotein; Sodium transport; Transport; Symport;
 MultiGene Family; Phosphorylation; Polymorphism.
 FT DOMAIN 1 11
 FT TRANSMEM 12 27
 FT TRANSMEM 28 59
 FT TRANSMEM 60 79
 FT TRANSMEM 80 81
 FT TRANSMEM 82 101
 FT TRANSMEM 102 110
 FT TRANSMEM 111 130
 FT TRANSMEM 131 134
 FT TRANSMEM 135 154
 FT TRANSMEM 155 180
 FT TRANSMEM 181 200
 FT TRANSMEM 201 209
 FT TRANSMEM 210 229
 FT TRANSMEM 230 249
 FT TRANSMEM 250 269
 FT TRANSMEM 270 298
 FT TRANSMEM 299 319
 FT TRANSMEM 320 339
 FT TRANSMEM 340 359
 FT TRANSMEM 360 366
 FT TRANSMEM 367 385
 FT TRANSMEM 386 435
 FT TRANSMEM 436 455
 FT TRANSMEM 456 832
 FT CARBOHYD 325 325
 FT VARIANT 144 144
 SQ SEQUENCE 832 AA: 92748 MW: 808887296C8F740 CRC64;

Query Match 17.0%; Score 471.5; DB 1; Length 832;
 Best Local Similarity 28.5%; Pred. No. 6.1e-23;
 Matches 148; Conservative 92; Mismatches 197; Indels 83; Gaps 19;

QY 22 VSEMNLEVALLCACIV-LGHLEENKWNESITALIIGCTGVIIILSGKSSHLVF- 79
 DB 56 IIALMLVAVLAKIVFHLH-KVTSVPESSALLIYGLVGLGIVL-----RADHIASPT 108
 QY 80 -SDLEFIIYLPPIFNAGQVKKKOFVNFMTIMFGAIGTISGSIISFGAVKIF--- 135
 DB 109 LTFVFEFIIYLPPIVDAGTFMNRFLFSSUGSILYAVGVNNAATGSLYGVLSG 168
 QY 136 --KHLDIDLFDFGYLAIGAIFATDSVCTLOYLSQ-DETPLLYSVFEQGVNDATSYV 192
 DB 169 IMGELKIGLDF---LLEFSLIAVDPVAVLAFVEEVHNEVFLIFEPESLINDAVTVV 225
 QY 193 LENAIGSEFMTSPDKIGLHF---TGNELYLFLSSFFLVGIGLCAVYIKKLYEGRHS 249
 DB 226 LYNVFSQFVTLGGDKVYGVDCVKGIVSFFVVSIGTIVGVFAFLSLVTR--FTKHVR 282
 QY 250 DREVALMLMLSYLSYMALEFYLSGITVFCGIVMSHTWHTVSSSVTTRHSPATLS 309
 DB 283 VIEPGVFIISYISLTSEKLSLSLILATFCGICCKQYKAKISQSQTVAITYTKMKMLA 342
 QY 310 FVAETFIPLVGMADALDIKMKFVKNSQGLSAVSSILVGLIVG--RAAFVPLSFLSN 367
 DB 343 SGAETIIFMFLGISAVDPILMTW-----NTAFVLTLLEVSYFRFAGVILQVWLIN 393
 QY 368 LAKKNSDKISFRQIILIMMAGLMGAVSIALAY---NKFTTSGHTSLHENAIMITSYV 423
 DB 394 RYRMVQLEIL--DOVVMSSYGGI-RGAVAFALVALDGNK-----VKEKNLEFVSTI 441
 QY 424 TVVLFSTVVGGLTKPLINLLPRHKOMPSGHSSMTSPSSPKHTVPLDNOPOSED 483
 DB 442 IYVFEFIIYQGLTIKPLVQML-----KYKSEHREPKLNEKGRADHIL-----SAIE 491
 QY 484 MITGPEVAPRTALMLLFRPTHTVHR-----WRKFDSPM 519
 DB 492 DISG-----QIGHNYLDRKMANFDRRL 514

RESULT 8

NAH3_RAT
 ID NAH3_RAT STANDARD: PRT: 831 AA.
 AC P26433:
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Sodium/hydrogen exchanger 3 (Na(+)/H(+) exchanger 3) (NHE-3).
 GN SLC9A3 OR NHE3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 ON NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Kidney;
 RX MEDLINE=92250539; Pubmed=1577762;
 RA Orlowski J., Kandasamy R.A., Shull G.E.;
 RT "Molecular cloning of putative members of the Na/H exchanger gene
 RT family. cDNA cloning, deduced amino acid sequence, and mRNA tissue
 RT expression of the rat Na/H exchanger NHE-1 and two structurally
 RT related proteins.";
 RL J. Biol. Chem. 267:9331-9339(1992).
 CC -I- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED
 CC BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL
 CC CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD
 CC SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL
 CC TRANSDUCTION.
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -I- TISSUE SPECIFICITY: MOST ABUNDANT IN COLON AND SMALL INTESTINE.
 CC -I- FOLLOWED BY KIDNEY AND STOMACH.
 CC -I- PTM: PHOSPHORYLATED (POSSIBLE).
 CC -I- SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.
 CC -I- CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC
 CC DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.
 CC -----
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 CC -----
 CC EMBL: M85300; AAA41702.1; -
 CC DR PIR: B40204; B40204.
 CC DR InterPro: IPR000676; NaH_Exchange.
 CC DR Pfam: PF00999; Na_H_Exchange; 1.
 CC DR PRINTS: PR01084; NAHEXCHNGR.
 CC KW Transmembrane; Glycoprotein; Sodium transport; Transport; Symport;
 CC MultiGene Family; Phosphorylation.
 CC FT DOMAIN 1 11
 CC FT TRANSMEM 12 25
 CC FT TRANSMEM 26 51
 CC FT TRANSMEM 52 70
 CC FT TRANSMEM 71 76
 CC FT TRANSMEM 77 96
 CC FT TRANSMEM 97 109
 CC FT TRANSMEM 110 130
 CC FT TRANSMEM 131 136
 CC FT TRANSMEM 137 157
 CC FT TRANSMEM 158 177
 CC FT TRANSMEM 178 199
 CC FT TRANSMEM 200 207
 CC FT TRANSMEM 208 229
 CC FT TRANSMEM 230 249
 CC FT TRANSMEM 250 271
 CC FT TRANSMEM 272 287
 CC FT TRANSMEM 288 306
 CC FT TRANSMEM 307 337
 CC FT TRANSMEM 338 359
 CC FT TRANSMEM 360 366
 CC FT TRANSMEM 367 387
 CC FT DOMAIN 388 402
 CC EXTRACELLULAR (POTENTIAL).
 CC A (M1) HYDROPHOBIC.
 CC CYTOPLASMIC (POTENTIAL).
 CC B (M2) HYDROPHOBIC.
 CC CYTOPLASMIC (POTENTIAL).
 CC C (M3) (POTENTIAL).
 CC EXTRACELLULAR (POTENTIAL).
 CC D (M4) (POTENTIAL).
 CC CYTOPLASMIC (POTENTIAL).
 CC E (M5) (POTENTIAL).
 CC EXTRACELLULAR (POTENTIAL).
 CC F (M5A) (POTENTIAL).
 CC CYTOPLASMIC (POTENTIAL).
 CC G (M5B) (POTENTIAL).
 CC EXTRACELLULAR (POTENTIAL).
 CC H (M6) (POTENTIAL).
 CC CYTOPLASMIC (POTENTIAL).
 CC I (M7) (POTENTIAL).
 CC EXTRACELLULAR (POTENTIAL).
 CC J (M8) (POTENTIAL).
 CC CYTOPLASMIC (POTENTIAL).
 CC K (M9) (POTENTIAL).
 CC EXTRACELLULAR (POTENTIAL).

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FT DOMAIN 403 423 L, HYDROPHOBIC.
FT DOMAIN 432 432 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 433 453 M (M10) (POTENTIAL).
FT DOMAIN 454 831 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 323 323 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 831 AA; 93105 MW; 77A4BF10DF9E3E CRC64;

Query Match 16.9%; Score 468.5; DB 1; Length 831;
Best Local Similarity 27.7%; Pred. No. 9.4e-23;
Matches 146; Conservative 89; Mismatches 200; Indels 93; Gaps 18;

QY 22 VSNMFLVALLCACIV-LGHLEENRWVESITALIIGLCTGYVLLSGKSSHLVLF-79
DB 54 IIALMILVASLAKIVFHLSH--KVTSVPEBAILIVGLVGLV-----WADHIASFT 106
QY 80 -SEDLFFLYLPPITFNAGFOYKKKQFFVNPMTIMLGAITGLISGAVKIPF---135
DB 107 LPTLFFLYLPPITVLDGYFMPKRLFPGNLGTLLVAVIGTINNAATGSLGVLSG 166
QY 136 --KHLIDFLDGDYLAIGAFATDSVCTLOVLSQ--DEPDLTSLVREGVNDATSVV 192
DB 167 LMGLKIGLDF--LIFGSLIAADVPAVLAVEEVHNVNLTIVFGESLMDAVTVV 223
QY 193 LENAQSFDMTSFDKIGLHF--IGNFLYLFSLSTFLGVGIGLCAVYIKKLYGRHST 249
DB 224 LYNVESFVTLGGDAVTVGDCVKIGVSPFVSLGTLGVIFAFLLSVTR--FTKHVR 280
QY 250 DREVALMMLSYLSIYMAELFYLSGILTFEFCGIVMSHYTHNNTBESSRVTTRSPATLS 309
DB 281 IIEPQFVVISLSTYLSIEMSLSAIILATFPCGCCOKRYVANISESATVRYTMKLA 340
QY 310 FVAETFFLYYGMALDLEKKMEVKNSSQGLSVAASSIIVGLILVGRAFVPELSESLMA 369
DB 341 SGAEITTFMFLGISAVDVIVMT-----MTAFVLLTVISYRAIGVVLQWILNRY 393
QY 370 KKNSSDKISFROQIITIMMARGAVSIALAYNKTFTSGHNSLHENAIMITSVTVLES 429
DB 394 RMVQLETT--DQVVMSTYSGL-RGAVAYALV---VLLDEKKVKEKNLFVSTTLIVVEFT 445
QY 430 TVVPELMKPLINILLPRHKQMPSSHSMTSSEPSK-----HETVPLDNDQP 478
DB 446 VTFQGLTKPLVQWL-----KVKRSEQREPLNEKLHGRADFHLASIED--- 490
QY 479 DSESDMITGPEVAREPTALRMLRPTHTVHRY---WRFQDSFMPRV 522
DB 491 -----ISG-----QIGHNYLMDKMNENPRKFLSKV 515

RESULT 9
NAHB_ONCMY STANDARD; PRT; 759 AA.
ID 001345;
AC 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-1999 (Rel. 38, Last annotation update)
DE Na(+)/H(+) exchanger beta (Na(+)/H(+) antiporter) (beta-NHE).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Nucleated erythrocyte;
RX MEDLINE=92357712; PubMed=1379718;
RA Borgese F., Sardet C., Cappadoro M., Pouyssegur J., Motaïs R.;
RT "Cloning and expression of a cAMP-activated Na+/H+ exchanger:
RT evidence that the cytoplasmic domain mediates hormonal regulation.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:6765-6769(1992).
CC -I- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED
CC BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL
CC CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD
CC SODIUM ION CHEMICAL GRADIENT.

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CC -I- SUBCELLULAR LOCATION: BASOLATERAL MEMBRANE.
CC -I- PTM: ACTIVATED BY CAMP, PROTEIN KINASE A AND PROTEIN KINASE C.
CC -I- MISCELLANEOUS: INHIBITED BY AMILORIDE AND 5-AMINO-SUBSTITUTED
CC DERIVATIVES AND ACTIVATED IN A COOPERATIVE FASHION BY
CC INTRACELLULAR H+.
CC -I- SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M94581; AAA49549.1; -
DR InterPro: IPR000676; NaH_Exchange; 1.
DR PRINTS: PR01084; NAHEXCHNGR.
KW Transmembrane; Glycoprotein; Sodium transport; Transport; Symport;
KW Multigene family; Phosphorylation.
FT DOMAIN 1 14 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 15 34 M1 (POTENTIAL).
FT DOMAIN 35 75 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 76 95 M2 (POTENTIAL).
FT DOMAIN 96 97 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 98 117 M3 (POTENTIAL).
FT DOMAIN 118 122 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 123 142 M4 (POTENTIAL).
FT DOMAIN 143 149 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 150 169 M5 (POTENTIAL).
FT DOMAIN 170 195 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 196 214 M5A (POTENTIAL).
FT DOMAIN 215 225 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 226 244 M5B (POTENTIAL).
FT TRANSMEM 245 261 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 262 282 M6 (POTENTIAL).
FT TRANSMEM 283 311 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 312 330 M7 (POTENTIAL).
FT TRANSMEM 331 352 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 353 372 M8 (POTENTIAL).
FT TRANSMEM 373 376 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 377 398 M9 (POTENTIAL).
FT DOMAIN 399 446 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 447 467 M10 (POTENTIAL).
FT DOMAIN 468 759 CYTOPLASMIC (POTENTIAL).
FT MOD_RES 641 641 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
FT MOD_RES 648 648 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
FT CARBOHYD 49 49 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 759 AA; 85173 MW; D6D95442995AE251 CRC64;

Query Match 16.9%; Score 468; DB 1; Length 759;
Best Local Similarity 28.2%; Pred. No. 9.2e-23;
Matches 148; Conservative 100; Mismatches 184; Indels 92; Gaps 22;

QY 31 LACAVILG-HLLEE-NRWVNESITALIIGLCTGYVLLSGKSSHLVFESEDLFFIYL 88
DB 78 LIALMILGHLHILPRLSAVPESCLLIYGLVGLIKVY-GEERPVV--DSQLEFLCL 133
QY 89 LPIIFNAGFOVKKQFFVNPMTIMLFGAIGTILS-----CSIISGAVKIFKH 137
DB 134 LPIIIDAGYFLRIPPTENVGTILVFAVIGTLMNAFFMGGLLYALCQIESVG----- 186
QY 138 LDIDFLDGDYLAIGAFATDSVCTLOVLSQF--TPILXSLYFSGGVNDATSVYLENA 196
DB 187 --LSGVDLACLFGSIVSAVDPAVALAVEETHINELVHIIIVFGESLINDAVTVLVNL 244
QY 197 IQSPD-----MTSPDKIGLHFNFLYLFSSFFLGAVGIGLCAVYIIRKLYGRHSTDR 252
DB 245 FEEFSKGVITVDVPLG--VVCFFVSLGVLVAIGVLAFLAFTSR---FTSHRYVE 298
QY 253 VALMMLMSYLSIYMAELFYLSGILTFEFCGIVMSHYTHNNTBESSRVTTRHSPATLSFVA 312

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Db 299 PLFVFLSYMAVLSSEMFHLSGIMALLACGVMPRYEANISHKSYTTIKYFLKMSVSS 358
OY 313 ETEFELYVGMAL---DIEKKKFKVNSOGLSVAASSILVGLVGRAPFEPFLSFLNLA 369
Db 359 ETLFIFELGVSFVGPANMNTFV-----LTVVI--LCLVSRVLGYIGLFIIN-- 405
OY 370 KKNSSDKISFROQIIMWAGIMRGAVSIALAVNFTSGHTSLHENAIMITSVTVLVS 429
Db 406 -KFRIVLTKKQDFIVAGGL-RGALAFSLGY--LLSNSQMRN---LFLAITTVLFT 458
OY 430 TVVGLMTKPLINLLPPHKMPSGHSSMTSEPPSKHFTVPLLDNQPDSESDMITGPE 489
Db 459 VFOGMPTRPLVELLAVKKK-----ESKPSINEIHTEFLDH-----LITGVE 502
OY 490 VARPALRMLRPTHTVHYRWYR---KEDDSFM-REVFGRGF 528
Db 503 -----GVCGHGHTHWKELNRFNKTYYKRWLIAGENF 535

RESULT 10
NAHL_RAT STANDARD; PRT; 820 AA.
AC P26431:
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Sodium/hydrogen exchanger 1 (Na(+)/H(+) exchanger 1) (NHE-1).
GN SLC9A1 OR NHE1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
ON NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY, TISSUE=Heart;
RX MEDLINE=92250339; PubMed=1577762;
RA Orlowski J., Kandasaamy R.A., Shull G.E.;
RT "Molecular cloning of putative members of the Na/H exchanger gene
RT family. cDNA cloning, deduced amino acid sequence, and mRNA tissue
RT expression of the rat Na/H exchanger NHE-1 and two structurally
RT -related proteins".
RL J. Biol. Chem. 267:9331-9339(1992).
CC -1- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED
CC BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL
CC CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD
CC SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL
CC TRANSDUCTION.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: NOT TISSUE SPECIFIC.
CC -1- PTM: PHOSPHORYLATED (POSSIBLE).
CC -1- SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.
CC -1- CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC
CC DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.
CC -1- CAUTION: HYDROPHOBIC DOMAINS A, B AND L ARE NOT BELIEVED TO BE
CC TRANSMEMBRANAL, BUT ONLY MEMBRANE-ASSOCIATED.
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CC entities requires a license agreement (See http://www.isb.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M65299; AAA98479.1; -.
DR PIR; A40204; A40204.
DR InterPro; IPR000676; NaH_Exchange.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR PRINTS; PR01084; NAHEXCHNGR.
KM Transmembrane; Glycoprotein; Sodium transport; Transport; Symport;
KM Multigene family; Phosphorylation.
FT DOMAIN 1 12 CYTOPLASMIC (POTENTIAL).

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FT DOMAIN 13 32 A (M1) HYDROPHOBIC.
FT DOMAIN 33 105 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 106 127 B (M2) HYDROPHOBIC.
FT DOMAIN 128 130 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 131 150 C (M3) (POTENTIAL).
FT DOMAIN 151 162 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 163 183 D (M4) (POTENTIAL).
FT DOMAIN 184 188 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 189 210 E (M5) (POTENTIAL).
FT DOMAIN 211 230 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 231 251 F (M5A) (POTENTIAL).
FT DOMAIN 252 260 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 261 282 G (M5B) (POTENTIAL).
FT DOMAIN 283 301 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 302 332 H (M6) (POTENTIAL).
FT DOMAIN 333 336 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 337 357 I (M7) (POTENTIAL).
FT DOMAIN 358 388 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 389 410 J (M8) (POTENTIAL).
FT DOMAIN 411 416 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 417 438 K (M9) (POTENTIAL).
FT DOMAIN 439 452 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 453 473 L, HYDROPHOBIC.
FT DOMAIN 474 482 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 483 503 M (M10) (POTENTIAL).
FT DOMAIN 504 820 N (M10) (POTENTIAL).
FT CARBOHYD 374 374 N-LINKED (GLCNAC...)(POTENTIAL).
SQ SEQUENCE 820 AA; 91647 MW; 58398DE74A9642FB CRC64;

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Query Match 16.9%; Score 467.5; DB 1; Length 820;
 Best local Similarity 28.0%; Pred. No. 1,le-22;
 Matches 143; Conservative 106; Mismatches 191; Indels 71; Gaps 20;

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OY 25 MNLFVALLACACVYGLHLEE-NRWNESTIALIIGLCVGVILLSSGKSHLVFSEDL 83
Db 109 ISLMILLACMKIGFVHVIPTISSIVPESCLIVGLVWG--LIVGVCETPPFL--QSDV 164
OY 84 FFIYLLPPIIFNFAFOVKKOFFVNMFTMLFGAIGTISCSITS--FGAVIFPHLDD 141
Db 165 FFIYLLPPIIDNGVYLPVROFTENIGTILFRAVGTLMNAFGLGLVAVCVGSDIN 224
OY 142 FIDFGDYLAIGAFPAATDSCTLOVLSODE-TPLYSLVFGGVNDATSVLFNAIOSF 200
Db 225 NIGLDTLTFEGSIISAVDPAVLAVEREIHNELHLIVFGSSLNDATVVLHLFEEF 284
OY 201 DMSSEPKGLH--FIG--NPLVPLSFVGLVGLCAIYIKKLYGRHSDEVALM 256
Db 285 ASLEY--VGISDIFLGSLFFVSVSLGVGVGVGVIAFTSR--FTSHIRVIEPLFV 338
OY 257 MNLASYIIMAEIFYLIGLTFVFCGIYVSHYTMHWNTSSRVTRHSPATLFAETFI 316
Db 339 FLTSYMAVLSAEFLHLSGIMALLASGVMPRYEANISHKSYTTIKYFLKMSVSELI 398
OY 317 FLYVGDALDIE--KMKFVNSOGLSVAASSILVGLVGRAPFEPFLSFLNLA 373
Db 399 FIFLGVSFVAGSHQWMTFV-----ISTLL--FCLIAVLGVILVLTPIIN--KFR 444
OY 374 SOKISFROQIIMWAGIMRGAVSIALAVNFTSGHTSLHENAIMITSVTVVLESTYVF 433
Db 445 IYKLPKDDPFIAYGGL-RGALAFSLGY--LIDKKHFPKCD--LFLAITTVLFTVQ 499
OY 434 GLMTKPLINLLPPHKMPSGHSSMTSEPPSKHFTVPLLDNQPDSESDMITGPEVARP 493
Db 500 GMTIRPLVDLAVKKKQ-----EIKRSINEIHQFLDH-----LITGIE----- 539
OY 494 TALRMLRPTHTVHYRWYR---KEDDSFMR 520
Db 540 -----DICGHYGHHWKDKLNRNKKYK 563

RESULT 11
NAHL_CRIGR STANDARD; PRT; 822 AA.
ID NAHL_CRIGR

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AC P48761:
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Sodium/hydrogen exchanger 1 (Na(+)/H(+) exchanger 1) (NHE-1).
 GN SLC9A1 OR NHE1.
 OS Cricetus griseus (Chinese hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetidae;
 OC Cricetus.
 OX NCBI_TaxID=10029;
 RN [1]
 RP SEQUENCE FROM N. A.
 RA MEDLINE-93192332; PubMed-8383540;
 RA Connillon L., Pouyssegur J.;
 RL Biochim. Biophys. Acta 1172:343-345(1993).
 CC -1- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL TRANSDUCTION.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- PTM: PHOSPHORYLATED (POSSIBLE).
 CC -1- SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.
 CC -1- CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.
 CC -1- CAUTION: HYDROPHOBIC DOMAINS A, B AND L ARE NOT BELIEVED TO BE TRANSMEMBRANAL, BUT ONLY MEMBRANE-ASSOCIATED.
 CC -----
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 CC -----
 CC EMBL: X68970; CAA8771.1; -
 DR InterPro: IPR000676; NaH_Exchngtr.
 DR Pfam: PF00999; Na_H_Exchange; 1.
 DR PRINTS: PR01084; NAHEXCHNGR.
 KW Transmembrane; Glycoprotein; Sodium transport; Transport; Symport;
 KW Multigene family; Phosphorylation.
 FT DOMAIN 1 12 CYTOPLASMIC (POTENTIAL).
 FT 13 32 A (M1) HYDROPHOBIC.
 FT DOMAIN 33 105 CYTOPLASMIC (POTENTIAL).
 FT 106 127 B (M2) HYDROPHOBIC.
 FT DOMAIN 128 130 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 131 150 C (M3) (POTENTIAL).
 FT DOMAIN 151 162 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 163 183 D (M4) (POTENTIAL).
 FT DOMAIN 184 188 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 189 210 E (M5) (POTENTIAL).
 FT DOMAIN 211 230 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 231 251 F (M5A) (POTENTIAL).
 FT DOMAIN 252 260 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 261 282 G (M5B) (POTENTIAL).
 FT DOMAIN 283 301 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 302 322 H (M6) (POTENTIAL).
 FT DOMAIN 323 336 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 337 357 I (M7) (POTENTIAL).
 FT DOMAIN 358 388 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 389 410 J (M8) (POTENTIAL).
 FT DOMAIN 411 416 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 417 438 K (M9) (POTENTIAL).
 FT DOMAIN 439 452 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 453 473 L, HYDROPHOBIC.
 FT DOMAIN 474 482 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 483 503 M (M10) (POTENTIAL).
 FT DOMAIN 504 822 CYTOPLASMIC (POTENTIAL).
 FT CAROHRD 374 374 N-LINKED (GLCNAc. . .) (POTENTIAL).
 SQ SEQUENCE 822 AA; 92003 MW; E97C1ACDAEB88DAA CRC64;

Query Match 16 9%; Score 467.5; DB 1; Length 822;
 Best Local Similarity 28.2%; Pred. No. 1,1e-22;
 Matches 144; Conservative 107; Mismatches 189; Indels 71; Gaps 21;
 25 MNLFVALLCACIYGLHLEE-NRWNESITALIIGCTGVILLISGKSSHLVFEEDL 83
 Db 109 ISLWILLACIMKIGFHVIPRISSIVESSCLLYGLLVGG--LIKVGSTPFL--QSDP 164
 QY 84 FFIYLLPPIIFNAGFOYKKQFFVNFMTIMLFGAIGTILSCSIIS--FQAVYIFKHLD 141
 Db 165 FFLFLPPIILDAGYFLPLRFQFENLGTILIFAVVGTLMNAFFLGLLYAVLVGGEQIN 224
 QY 142 FLDFGVIALGATFAANDSCITQVLSODE-PFLTSLVFGEGVANDSVYLEFNAIQSF 200
 Db 225 NIGLDLFLFGSIISADPAVAVAVEEIHINELLIVFGESLDANDATVYLHFEF 284
 QY 201 DMTSFPKIGLH--FTIG--NFLYFLSFTPLGVGIGLCAVYIKKLYFRSHSTREVALM 256
 Db 285 --ANYD-SIGISDPLIGLSFFVVALGVGVGVYIAFTSR--FTSHIRVIEPLFV 338
 QY 257 MMSYLSYIAELFYISGLITVFCCIVMSHYTHWAVTESKRTTTHSATLSFAVETI 316
 Db 339 FLVSVAYLSEAEFLHLSGVALIASGVMPRYEAMISHSHTTIKYFLKMSVSETLI 398
 QY 317 FLVYGMALDIE---KMKFYKNSQGLSAVSSILVGLIVGRAAFVFPFLSLNLAKNS 373
 Db 399 FIFGVSTVAGSHQWNTFY-----ISTLL--FCLIRVLGVVLWTFIN---KFR 444
 QY 374 SDRISFRQOIIWAGIMRGAVSIALAYNKFTTSGHTSLHENAIMTSTVYVLSFTVVF 433
 Db 445 IVKTLPRDQFLTAVGGL--RGALAFSLGY--LMDKHFPMCD--LFLTAITVYVFFVFO 499
 QY 434 GLMKPLINLLPPIHMQPGHSGHSMITSEPSKHTVPLDQNPQSDMTIGPVAP 493
 Db 500 GMTIRPLVDLLAAKKQ-----ETKRSINEEIHQFLD-----LLTGE----- 539
 QY 494 TALRMLRTPTHTVRYWR---KFDSPFR 520
 Db 540 -----DIGHGHHMKDKLRFNKRYK 563
 RESULT 12
 NAH3.DIDMA STANDARD; PRT: 839 AA.
 ID NAH3.DIDMA
 AC Q28362;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Sodium/hydrogen exchanger 3 (Na(+)/H(+) exchanger 3) (NHE-3).
 GN SLC9A3 OR NHE3.
 OS Didelphis marsupialis virginiana (North American opossum).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
 OX NCBI_TaxID=9267;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-95358256; PubMed-7631739;
 RA Aremiya M., Yamaji Y., Cano A., Moe O.W., Alpern R.J.;
 RT "Acid incubation increases NHE-3 mRNA abundance in OKP cells.";
 RL Am. J. Physiol. 269:C126-C133(1995).
 CC -1- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL TRANSDUCTION.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- PTM: PHOSPHORYLATED (POSSIBLE).
 CC -1- SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.
 CC -1- CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.
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FT TRANSMEM 370 390 K (M9) (POTENTIAL).
FT DOMAIN 391 405 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 406 426 L, HYDROPHOBIC.
FT DOMAIN 427 435 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 436 456 M (M10) (POTENTIAL).
FT DOMAIN 457 834 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 326 326 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 834 AA; 92907 MW; 3E7CE33D65DF36F7 CRC64;

Query Match 16.7%; Score 461; DB 1; Length 834;
Best Local Similarity 28.6%; Pred. No. 2,8e-22;
Matches 140; Conservative 85; Mismatches 197; Indels 68; Gaps 15;

QY 48 VNESTALIIIGLCTGVVLLISGKSSHLV--SEDFIYLLPPIIFNAGFOYKKQF 105
DB 82 VPESALLIVGLVIGIV-----MAADHIASTPLIPYFFYLLPPIVLADGYEMPMLF 136
QY 106 FVNFMIMFGAIGFICSTISFGAVKIF-----KHIDIFLDGDIATGATFATDS 160
DB 137 FGNLTITLLIYAVGVVMAATIGLSLYGVFLSGLMGDIQIGLDP--LFGSLMAADP 193
QY 161 VCTLOVLSQ-DETPLLYSLVGEVVDATSVYFNAIQSPDMTSFDPKIGLHF--IGN 216
DB 194 VAVLAVFESEVHNEVLEFIVEGESLNDAYVVLXNVESEFVALGDNVTVGDCVKIYS 253
QY 217 FLYELSLFFLGIVGIGLCATITIKLYGRSHSTDEVALMMLMSTLSTIMAEFLYSGIL 276
DB 254 FVVVSLIGGLVGVVAFPLISLVTR--PTKHVRIIEPGFVFIISLYSLTSEMSTSLIL 310
QY 277 TVEFGIYVMSHTVMTNHESSRVTRHSEFATLSFEVETFIYVGMDDLIEKKMFYVNS 336
DB 311 AITFGICQCKYKKNISQSKATVRYTKMKLASSAEITIFELGISAVNPFIWTV---- 366
QY 337 OGLSAVSSIIIVGLLYGRAAFVPLSPLSLNKKNSDKISFRQIITIMAGLMRGAVS 396
DB 367 ---NNAFVLLTFLVFSYRAIGVVLQTWLNNRYMVGLEPI--DQVVLVSGLL-RGAVA 419
QY 397 IALANKFTTSHTSLHERALMITSTVTVVLFSTYVFGMLKPLINLLPHKQMPSHS 456
DB 420 FALV---VLLDGDVKRKKNLFVSTPIIVFETVFOGLITLKPLVQWL---KKARSEHR 471
QY 457 SMTSESPSKFTVPLDNDQPSDMITGPEVARPTALRLRLPTHTVARY----WR 512
DB 472 ERLMELKLGRAFDHIL-----SAIEDISG-----QIGHNITLRDQWS 508
QY 513 KPDSFMRPV 522
DB 509 HDRKFLSRV 518

RESULT 14
ID NAHL_PIG STANDARD; PRT; 818 AA.
AC P48762;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Sodium/hydrogen exchanger 1 (Na(+)/H(+) exchanger 1) (NHE-1).
GN SLC9A1 OR NHE1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9833;
[1]
RP SEQUENCE FROM N.A.
RA MEDLINE=92087905; PubMed=1661081;
RA Reilly R.F., Hildebrandt F., Bismesderfer D., Sargent C.,
RA Pouyssegur J., Aronson P.S., Slayman C.W., Igarashi P.;
RT "cDNA cloning and immunolocalization of a Na(+)-H+ exchanger in
RT LLC-PK1 renal epithelial cells.";
RL Am. J. Physiol. 261:F1088-F1094(1991).
CC -I- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED

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CC BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL
CC CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD
CC SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL
CC TRANSDUCTION.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- PTM: PHOSPHORYLATED (POSSIBLE).
CC -I- SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.
CC -I- CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC
CC DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.
CC -I- CAUTION: HYDROPHOBIC DOMAINS A, B AND L ARE NOT BELIEVED TO BE
CC TRANSMEMBRANAL, BUT ONLY MEMBRANE-ASSOCIATED.
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CC or send an email to license@isb-sdb.ch).
CC -----
DR EMBL: M89631; AAA31093.1; -.
DR EMBL: S71135; AAB20633.1; -.
DR InterPro: IPR000676; NaH_Exchange.
DR Pfam: PF00999; Na_H_Exchange; 1.
DR PRINTS: PR01084; NAHEXCHNGR.
KW Transmembrane; Glycoprotein; Sodium transport; Transport; Symport;
KW Multigene family; Phosphorylation.
FT DOMAIN 1 11 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 12 31 A (M1) HYDROPHOBIC.
FT DOMAIN 32 101 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 102 123 B (M2) HYDROPHOBIC.
FT DOMAIN 124 126 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 127 146 C (M3) (POTENTIAL).
FT TRANSMEM 147 158 D (M4) (POTENTIAL).
FT TRANSMEM 159 179 E (M5) (POTENTIAL).
FT TRANSMEM 180 184 F (M5) (POTENTIAL).
FT TRANSMEM 185 206 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 207 226 F (M5A) (POTENTIAL).
FT TRANSMEM 227 247 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 248 256 G (M5B) (POTENTIAL).
FT TRANSMEM 257 278 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 279 297 H (M6) (POTENTIAL).
FT TRANSMEM 298 318 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 319 332 I (M7) (POTENTIAL).
FT TRANSMEM 333 353 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 354 384 J (M8) (POTENTIAL).
FT TRANSMEM 385 406 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 407 412 K (M9) (POTENTIAL).
FT TRANSMEM 413 434 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 435 448 L, HYDROPHOBIC.
FT TRANSMEM 449 469 L, HYDROPHOBIC.
FT TRANSMEM 470 478 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 479 499 M (M10) (POTENTIAL).
FT TRANSMEM 500 818 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 370 370 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 683 683 H -> Y (IN REF. 1; AAB20633).
SQ SEQUENCE 818 AA; 90987 MW; 9329F79A51D3DC9 CRC64;

Query Match 16.6%; Score 460.5; DB 1; Length 818;
Best Local Similarity 28.0%; Pred. No. 3e-22;
Matches 145; Conservative 108; Mismatches 181; Indels 83; Gaps 22;

QY 25 MNLFVALLCACIVGHLEE-NRMVNSITALLIGCTGVVLLISGKSSHLVSEDL 83
DB 105 ISMLILACLAKIGFHVHPIPTISIVPESCLLIYVGLVGLIAV--GETPPPL--QSEY 160
QY 84 FFYLIPPIIFNAGFOYKKQFVNFTIMFGAIGLISCSITIS--FGAVKIFKHLDID 141
DB 161 FFLFLPPIILDAGYFLPLKQFTENGLTILIFAVGIMNAFVLGIMAVCLVGEQIN 220
QY 142 FLDFGDIATGATPAATDSVCTLOVLSQDE--FPLVSLVFGESVVDATSVYFNAIQSF 200
DB 221 NIGLDMLFGSIIISAVDPAVLAIVEEIHINELHILVFGESLNDAYVVLXHYHLEEF 280

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QY	201	DWTSFDPKIG-----LH7IGNEVLFLSTSPFLGIGLGLCAIYIIKKILYFGRHSDREVAL	255
Db	281	--AND-RGVLDYDVLGLF-SFEVWSJGAGVGVGVYIAETSR---FTSHIRVTEPLF	333
QY	256	NMLMSYLSYINAAELFEYLSGLITLVFECGIVSMHYVMHWNTESRYVTRHSFATLSFEVAET	315
Db	334	VFLYSYMAVLSAEELFHSIGIMALLASGVMMRYPEANISHSHTTIKYLKMSVSSETL	393
QY	316	IFLYVGMALDIE---KKKFKNSOGSLVAVSSILVGLILVGRAAFVPLSPLSNLAKN	372
Db	394	IFIFIGVSTVAGSHMMNTFV-----ISTLL--FCLLIARVLGVLGTWFIN---KF	439
QY	373	SSDKISFROQIIIMWAGIMRGAVSIALAYNNFTTSGHSLHEN-----AMISTVYVVL	427
Db	440	RIVKILTPEDOFILAVGL--KALINFSL-----GH-LDKNHPKCDLFRAITIVIF	489
QY	428	FSTVVEGLMTRPLINLLRPRKQMPSGHSSMTTSEPPSPKHFYPLLDNOPDSESDMTG	487
Db	490	FTEVQGTIRPLVDLLAVKKQ-----ETKRSINEIHQFLDH-----LITG	533
QY	488	PEVARPTALRMLRPTTVIRYR-----KEDSFMR	520
Db	534	IE-----DICGHYGHNNKMDKLNREKKYVK	559
RESULT 15			
ID	NAHL_RABIT	STANDARD:	PRT: 816 AA.
AC	P23791;		
DT	01-NOV-1991 (Rel. 20, Created)		
DT	01-NOV-1991 (Rel. 20, Last sequence update)		
DE	30-MAY-2000 (Rel. 39, Last annotation update)		
DN	Sodium/hydrogen exchanger 1 (Na(+)/H(+) exchanger 1) (NHE-1).		
GN	SIC9A1 OR NHE1.		
OS	Oryctolagus cuniculus (Rabbit).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.		
OX	NCBI_TaxID:9986;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	- STRAIN=NEW ZEALAND WHITE; TISSUE=ileal villus;		
RX	MEDLINE=91293066; PubMed=1712287;		
RA	Tse C.-M., Ma A.-I., Yang Y.W., Watson A.J.M., Levine S.,		
RA	Montrose M.H., Potter J., Sarder C., Pouyssegur J., Donowitz M.,		
RT	"Molecular cloning and expression of a cDNA encoding the rabbit ileal		
RT	"villus cell basolateral membrane Na ⁺ /H ⁺ exchanger.";		
RL	EMBO J. 10:1957-1967(1991).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Kidney.		
RX	MEDLINE=92096447; PubMed=1661611;		
RA	Hildebrandt F., Pizzonia J.H., Rellly R.F., Reboucas N.A.,		
RA	Sardet C., Pouyssegur J., Slayman C.W., Aronson P.S., Igarashi P.;		
RT	"Cloning, sequence, and tissue distribution of a rabbit renal Na ⁺ /H ⁺		
RT	exchanger transcript.";		
RL	Biochim. Biophys. Acta 1129:105-108(1991).		
RN	[3]		
RP	SEQUENCE OF 472-816 FROM N.A.		
RC	STRAIN=NEW ZEALAND WHITE; TISSUE=Heart muscle;		
RX	MEDLINE=9118752; PubMed=170485;		
RA	Fliegel L., Sardet C., Pouyssegur J., Barr A.;		
RT	"Identification of the protein and cDNA of the cardiac Na ⁺ /H ⁺		
RT	exchanger.";		
RL	FEBS Lett. 279:25-29(1991).		
CC	-1- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED		
CC	BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL		
CC	CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD		
CC	SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL		
CC	TRANSDUCTION.		
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.		
CC	-1- TISSUE SPECIFICITY: KIDNEY AND INTESTINE.		
CC	-1- PTM: PHOSPHORYLATED (POSSIBLE).		

```

CC -1- SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.
CC -1- CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC
CC DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sdb.ch/announce/
CC or send an email to license@isb-sdb.ch).
CC -----
DR EMBL; X59395; CAA42558.1; -
DR EMBL; X61504; CAA43721.1; -
DR EMBL; X56536; CAA39881.1; -
DR PIR; S13926; S13926.
DR PIR; S16328; S16328.
DR InterPro; IPR000676; Nah_Exchange.
DR Pfam; PF00999; Nah_H_Exchange; 1.
DR PRINTS; PR01084; NAHEXCHNGR.
KM Transmembrane; Glycoprotein; Sodium transport; Transport; Symport;
KV Multigene family; Phosphorylation.
FT DOMAIN 1 15
FT TRANSMEM 16 35
FT TRANSMEM 36 107
FT TRANSMEM 108 127
FT TRANSMEM 128 129
FT TRANSMEM 130 149
FT TRANSMEM 150 154
FT TRANSMEM 155 174
FT TRANSMEM 175 191
FT TRANSMEM 192 211
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FT TRANSMEM 407 410
FT TRANSMEM 411 430
FT TRANSMEM 431 480
FT TRANSMEM 481 500
FT TRANSMEM 501 816
FT CARBOHYD 75 75
FT CARBOHYD 370 370
FT CONFLICT 242 242
FT CONFLICT 569 569
SQ SEQUENCE 816 AA; 90717 MW; 336738D267FEF436 CRC64;
Query Match 16.6%; Score 459.5; DB 1; Length 816;
Best Local Similarity 28.2%; Pred. No. 3.5e-22;
Matches 144; Conservative 105; Mismatches 191; Indels 71; Gaps 20.
QY 25 MNLFVALLCAGIVLGLDEE-NRWYNESITALLIGCTGVVILLISGKSSHILVFSDDL 83
DB 105 ISLWILLACLMKIGRHVPTISISYPESCLLVGLVGLIKGV-GEKRPPL---QSEV 160
QY 84 FFYIILPPIIFNAGQVKKKQFFVFMIMLFGAIGTILSCITIS--FGAVKIFKHLID 141
DB 161 FFLFLPPIIDAGFLRLROFTENLGTLLIFAVVGLTMAAFGLGLMAYCLVGGEOIN 220
QY 142 FLDFEDYLAIGAIFATPSVCTLOVLSODE-PLLYSLVFGGVNDATSVLFNAIOSF 200
DB 221 NIGLLDNLLFGSITISAVDPVAVLAFEEIHRELHLIIVFGSLNDADVIVLYHLEEF 280
QY 201 DMTSFD---PKIGHFTGNFLYLELSSFTFLVGIGLCAVITIKKLYGGRHSTDREVAL 256
DB 281 --ANDYHGIYDIVLGF-LSEFVVALGVGVGVYVAVTAFTSR--FPAHRIVIEPLEV 334

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OY 257 MUMSYIYMAELPFLSGILVFPQIYMSHYTMHNWTESSRYVTRHSPATLSPVAETFI 316
DB 335 FLYSTMAFLSAELPFLSGIMALIASGVMPRYEANISHKSHTTIKYFLKMWSSVSETLI 394
OY 317 FLYVGMALDIE--KMKFYKNSOGLSYAVSSIIWGLILVGRAAFVFPPLSFLSNLARKNS 373
DB 395 FIFLGVSIVAGSHHNMWTFV-----ISTLL-FCLTARVGLGLTWFIN--KFR 440
OY 374 SOKISFROQIIIMWAGLMRGAVSTALAYNKFTTSGHTSLHENAIMITSTVTVLSTVVF 433
DB 441 IVKLPKDOFLIAYGGL-RGAIAFSLGY-LIDKKNHPPMD-LFLTAITVIFEFTVYVQ 495
OY 434 GLMTPKPLINLLPRPKOMPSGHSMTSESPSKHFTVPLDNDQPDSESDMITGPEYARP 493
DB 496 GMTIRPLVDLAVKKQ-----ETKRSINEIHTQFIDH-----LITGIE---- 535
OY 494 TALRMLLRTPTHTVHRVYR---KFDSPMR 520
DB 536 -----DICGHYGHMHMKDKLNRFNKKYVK 559

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Search completed: October 18, 2002, 12:26:10
 Job time : 19 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 18, 2002, 12:24:10 : Search time 15 Seconds

(without alignments) 882.578 Million cell updates/sec

Title: US-09-830-123-2

Perfect score: 2768

Sequence: 1 MAFGLSSILQNSDLFTSDHA.....FGGRGFVFPVAGSPVEGSPR 542

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*

1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*

2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*

3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*

4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*

5: /cgn2_6/ptodata/1/1aa/PCtUS.COMB.pep:*

6: /cgn2_6/ptodata/1/1aa/backfill1es1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	471.5	17.0	832	2	US-08-677-734A-12
2	468.5	16.9	831	2	US-08-677-734A-11
3	461	16.7	834	2	US-08-677-734A-9
4	461	16.7	834	2	US-08-677-734A-10
5	112.5	4.1	438	2	US-08-677-049-9
6	109.5	4.0	1394	4	US-09-213-053-2
7	106	3.8	635	2	US-09-014-969-11
8	100	3.6	775	2	US-08-714-070A-1
9	99	3.6	584	2	US-08-928-692-13
10	97.5	3.5	352	3	US-08-466-343D-2
11	97.5	3.5	352	4	US-09-087-232A-13
12	97.5	3.5	352	4	US-08-861-105-14
13	97.5	3.5	352	4	US-08-575-967A-2
14	97.5	3.5	352	4	US-09-045-583-52
15	96	3.5	664	4	US-09-268-140-2
16	95.5	3.5	370	4	US-09-144-914-8
17	95	3.4	1786	4	US-08-477-451-16
18	93.5	3.4	397	1	US-08-098-141-2
19	92.5	3.3	326	4	US-08-986-768-2
20	92.5	3.3	513	4	US-09-097-889-15
21	92.5	3.3	3287	2	US-08-477-451-7
22	91.5	3.3	299	2	US-09-097-759-3
23	91.5	3.3	306	2	US-09-097-759-2
24	91.5	3.3	649	4	US-08-800-291B-6
25	91.5	3.3	650	4	US-08-800-291B-4
26	91	3.3	342	3	US-08-852-824-2
27	90.5	3.3	360	4	US-08-875-573-20

28	90.5	3.3	360	4	US-09-232-878-2	Sequence 2, Appl1
29	90.5	3.3	360	4	US-09-045-583-55	Sequence 55, Appl1
30	90.5	3.3	461	2	US-08-672-814D-2	Sequence 2, Appl1
31	90.5	3.3	461	4	US-09-333-696-2	Sequence 2, Appl1
32	90	3.3	266	2	US-08-225-480-7	Sequence 7, Appl1
33	90	3.3	266	2	US-09-097-759-4	Sequence 4, Appl1
34	90	3.3	916	2	US-08-928-692-58	Sequence 58, Appl1
35	89.5	3.2	664	2	US-08-895-522-4	Sequence 4, Appl1
36	89.5	3.2	634	2	US-09-195-391-4	Sequence 4, Appl1
37	89	3.2	355	1	US-08-461-244-2	Sequence 4, Appl1
38	89	3.2	355	4	US-09-045-583-56	Sequence 56, Appl1
39	88	3.2	506	4	US-09-066-047-7	Sequence 7, Appl1
40	88	3.2	524	2	US-08-928-692-12	Sequence 12, Appl1
41	88	3.2	1334	2	US-08-896-545-2	Sequence 2, Appl1
42	88	3.2	1334	4	US-09-328-020-2	Sequence 2, Appl1
43	87.5	3.2	411	4	US-09-236-080-6	Sequence 6, Appl1
44	87.5	3.2	649	4	US-08-800-291B-5	Sequence 5, Appl1
45	87	3.1	459	4	US-09-097-889-22	Sequence 22, Appl1

ALIGNMENTS

RESULT 1
US-08-677-734A-12

Sequence 12, Application US/08677734A

Patent No. 5871919

GENERAL INFORMATION:

APPLICANT: Brant, Steven R.

APPLICANT: Yun, Chris C.H.

APPLICANT: Donowitz, Mark

APPLICANT: Tse, Chung-Ming

TITLE OF INVENTION: Cloning, Tissue Distribution, and

TITLE OF INVENTION: Functional Analysis Of The Human Na/H+ Exchanger Isoform,

NUMBER OF INVENTION: NHE3.

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

ADDRESS: 1300 I Street, N.W., Suite 700

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/677,734A

FILING DATE: 10-JUL-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Fordis, Jean B.

REGISTRATION NUMBER: 32,984

REFERENCE/DOCKET NUMBER: 05387.0043-00000

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 408-4000

TELEFAX: (202) 408-4400

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 832 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-677-734A-12

Query Match 17.0%; Score 471.5; DB 2; Length 832;
Best Local Similarity 28.4%; Pred. No. 3,6e-38;
Matches 147; Conservative 92; Mismatches 200; Indels 79; Gaps 18;

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/677,734A
FILING DATE: 10-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fordis, Jean B.
REGISTRATION NUMBER: 32,984
REFERENCE/DOCKET NUMBER: 05387, 0043-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 834 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-677-734A-9

Query Match 16.7%; Score 461; DB 2; Length 834;
Best Local Similarity 28.6%; Pred. No. 4e-37;
Matches 140; Conservative 85; Mismatches 197; Indels 68; Gaps 15;

QY 48 VNESTALIIIGCTGVVILLSSGKSSHLVF--SEDLFFIYLLPPIIFNAGFOVKKQF 105
DB 82 VPESALLIVGLVIGIV-----WADHIASFTLPTVFYFFYLLPPIVLDAGYFMPNRLF 136
QY 106 FVNEMTIMGALIGTLLSCSIISFGAVKIF----KHLIDFLDFGDIYLAIGAFATDS 160
DB 137 FGNLGTILLVAVGVWMAATGSLYGVFTLSGLMGDIQIGLDF--LFGSLMAAVDP 193
QY 161 VCTIQVLSQ-DETPLLSLVFGEGVNDATSVLFNAIQSFDMTSFDPKIGLHF--IGN 216
DB 194 VAVLAVEEVHVNVEVLIIFEGESLNDATVVLNVNFEFVALGDNVYGVDCVKGIVS 253
QY 217 FLYLFSLSTFLGVGIGLCAIYIKKLYFGHSTDEVALMMLMSTYLSIMAEFLYSGIL 276
DB 254 FFVYSLGIGLVGVAFILSLVTR---FTKHVRIIEPGEFVFIISYLSYLSSEMLSLAIL 310
QY 277 TVEFCGIWMSHYTMHNWTESSRVTRHSFATLSFVAETFIYLVGMADLIEKKKFKVNS 336
DB -311 AITFCGICCKYKANISEQSATTVRYTKMKMLASAEITIIEMFLGISAVNPFIMTW--- 366
QY 337 OGLSVAVSSILVGLILVGRAAFVPLSPLSNLAKKSSDKISFRQOIIIMWAGLMRGAVS 396
DB 367 ---NTAFVLLTLVFIISYRAIGVLTQWLNRYRMVQLEPI---DQVVLSTYGL-RGAVA 419
QY 397 IALAANKFTSGHSLHENAIMITSVTVVLFSTVYFGLMKPLINLLPPHKOMPSGHS 456
DB 420 FALV---VLLDGDKVKKKNLEFVSTIIIVFEFTYFQGLTIKPLVQWL---KVKRSEHR 471
QY 457 SMTSESPSPKHFVPLLDNQPDSEDMITGPEVAPRTALMLRLPTHTVHRY---WR 512
DB 472 EPRLNELKGRAPDHL-----SAIEDISG-----QIGHNLYLDRKWS 508
QY 513 KFDSEFMRPV 522
DB 509 HFDRKFLSRV 518

RESULT 4
US-08-677-734A-10
Sequence 10, Application US/08677734A
Patent No. 5871919
GENERAL INFORMATION:
APPLICANT: Brant, Steven R.
APPLICANT: Yuen, Chnls C.H.
APPLICANT: Donowitz, Mark

APPLICANT: Tse, Chung-Ming
TITLE OF INVENTION: Cloning, Tissue Distribution, and
TITLE OF INVENTION: Functional Analysis Of The Human Na+/H+ Exchanger Isoform,
TITLE OF INVENTION: NHE3.
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunnet
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/677,734A
FILING DATE: 10-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fordis, Jean B.
REGISTRATION NUMBER: 32,984
REFERENCE/DOCKET NUMBER: 05387, 0043-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 834 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-677-734A-10

Query Match 16.7%; Score 461; DB 2; Length 834;
Best Local Similarity 28.6%; Pred. No. 4e-37;
Matches 140; Conservative 85; Mismatches 197; Indels 68; Gaps 15;

QY 48 VNESTALIIIGCTGVVILLSSGKSSHLVF--SEDLFFIYLLPPIIFNAGFOVKKQF 105
DB 82 VPESALLIVGLVIGIV-----WADHIASFTLPTVFYFFYLLPPIVLDAGYFMPNRLF 136
QY 106 FVNEMTIMGALIGTLLSCSIISFGAVKIF----KHLIDFLDFGDIYLAIGAFATDS 160
DB 137 FGNLGTILLVAVGVWMAATGSLYGVFTLSGLMGDIQIGLDF--LFGSLMAAVDP 193
QY 161 VCTIQVLSQ-DETPLLSLVFGEGVNDATSVLFNAIQSFDMTSFDPKIGLHF--IGN 216
DB 194 VAVLAVEEVHVNVEVLIIFEGESLNDATVVLNVNFEFVALGDNVYGVDCVKGIVS 253
QY 217 FLYLFSLSTFLGVGIGLCAIYIKKLYFGHSTDEVALMMLMSTYLSIMAEFLYSGIL 276
DB 254 FFVYSLGIGLVGVAFILSLVTR---FTKHVRIIEPGEFVFIISYLSYLSSEMLSLAIL 310
QY 277 TVEFCGIWMSHYTMHNWTESSRVTRHSFATLSFVAETFIYLVGMADLIEKKKFKVNS 336
DB 311 AITFCGICCKYKANISEQSATTVRYTKMKMLASAEITIIEMFLGISAVNPFIMTW--- 366
QY 337 OGLSVAVSSILVGLILVGRAAFVPLSPLSNLAKKSSDKISFRQOIIIMWAGLMRGAVS 396
DB 367 ---NTAFVLLTLVFIISYRAIGVLTQWLNRYRMVQLEPI---DQVVLSTYGL-RGAVA 419
QY 397 IALAANKFTSGHSLHENAIMITSVTVVLFSTVYFGLMKPLINLLPPHKOMPSGHS 456
DB 420 FALV---VLLDGDKVKKKNLEFVSTIIIVFEFTYFQGLTIKPLVQWL---KVKRSEHR 471
QY 457 SMTSESPSPKHFVPLLDNQPDSEDMITGPEVAPRTALMLRLPTHTVHRY---WR 512
DB 472 EPRLNELKGRAPDHL-----SAIEDISG-----QIGHNLYLDRKWS 508

OY 513 KPDSDPMRPV 522
 DB 509 HPRKFLSRV 518

RESULT 5

US-08-677-049-9
 ; Sequence 9, Application US/08677049
 ; Patent No. 5858707
 ; GENERAL INFORMATION:
 ; APPLICANT: Guimaraes, M. Jorge
 ; APPLICANT: Bazan, J. Fernando
 ; APPLICANT: McClanahan, Terrill K.
 ; APPLICANT: Zlotnik, Albert
 ; TITLE OF INVENTION: PURIFIED MAMMALIAN NUCLEOBASE PERMEASES;
 ; TITLE OF INVENTION: NUCLEIC ACIDS; ANTIBODIES
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DNAX Research Institute
 ; STREET: 901 California Avenue
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94304-1104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/677,049
 ; FILING DATE: 03-JUL-1996
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/000,788
 ; FILING DATE: 03-JUL-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ching, Edwin P.
 ; REGISTRATION NUMBER: 34,090
 ; REFERENCE/DOCKET NUMBER: DX0511
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-852-9196
 ; TELEFAX: 415-496-1200
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 438 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; FEATURE:
 ; NAME/KEY: Region
 ; LOCATION: 115..144
 ; OTHER INFORMATION: /note= "Encompasses TM 4 of Figure
 ; OTHER INFORMATION: 4"
 ; FEATURE:
 ; NAME/KEY: Region
 ; LOCATION: 323..357
 ; OTHER INFORMATION: /note= "Encompasses TM 9 of Figure
 ; OTHER INFORMATION: 4"
 ; FEATURE:
 ; NAME/KEY: Region
 ; LOCATION: 359..386
 ; OTHER INFORMATION: /note= "Encompasses TM 10 of Figure
 ; OTHER INFORMATION: 4"
 ; US-08-677-049-9

Query Match 4.1%; Score 112.5; DB 2; Length 438;
 Best Local Similarity 22.1%; Pred. No. 0.0076;
 Matches 103; Conservative 69; Mismatches 153; Indels 141; Gaps 25;
 OY 56 IIGICTGVVILLSGKSSHLVFSDDLFIYLLPPIIFNAG----FQVKKKQFVNPMPT 111

DB 16 VIANMGAIVVPLVYGKAMGLV--EQL--TYLVSIDIFKCGVATLLQVWSNRFEGIGLP 71
 OY 112 IML---FGAIGTLISC-----SITSGCAVAFKHLIDIDFPGDYLAIGAF-- 155
 DB 72 VVLGCTPTAVSPMAIGSEYGVSTVYGSIIASGILVL---ISFF-FKLV---SFFPP 123
 OY 156 AATDSVCTLOVLSODETPL-LYSLVFGEGVFN--DATSVVLFNAIQSPMTSHPKRGH 212
 DB 124 VTGGSVVT--TIGITLMPVAMNMGAGGSADGDSLNALATVTSIIV----- 171
 OY 213 FIGNFLYFLS-----STPLGVGIGLCAVYIKKLYFGHSTDRVALMIMSYLSYM 266
 DB 172 ---LTVFTKGFIVKSVLIGLIGFTIAYFGMKVQFDVSD---AAVQMIGPFYEG 223
 OY 267 AELFYSLGILTFPCGVYMSHYTMWNTESRVTTHSPATLSFVAETFLFLYGV----- 321
 DB 224 APSEHAPITMTSIVAVL-----SLVSTGVYFALGDLINR 259
 OY 322 -MDALDEKKKFKVNSQGLSAVSSILVGLVGRAAFVP--LSPLSLA-----KKN 372
 DB 260 RLTEIDLSKG---YRAGLAV-----LLGCIFFNAFPYTAFGONVGLVGTGKKN 306
 OY 373 S-----SDKISFRQOII--IWWAGIMRGAVSIALAVN-KFTTSGHTSLHEN 415
 DB 307 AVIVVTGVIIIMAFGLFEPKIAAFTTIIPSVAVLGGAMVAMEGMVAYGIKMLRIDFAKOE 366
 OY 416 AIMTSTVTVVLSTVYVFGIATKPLINLLPPIKOMPSSGHSMTS 461
 DB 367 LLIVACSVGLGLVTVVPDIF-----KQLPSALTLLITN 400

RESULT 6

US-09-213-053-2
 ; Sequence 2, Application US/09213053
 ; Patent No. 6159477
 ; GENERAL INFORMATION:
 ; APPLICANT: AUDONNET, Jean-Christophe
 ; APPLICANT: BAUDU, Philippe
 ; TITLE OF INVENTION: CANINE HERPESVIRUS BASED RECOMBINANT LIVE VACCINE, IN
 ; TITLE OF INVENTION: PARTICULAR AGAINST CANINE DISTEMPER, RABIES OR THE
 ; TITLE OF INVENTION: PARAINFLUENZA 2 VIRUS
 ; FILE REFERENCE: 454313-2200
 ; CURRENT APPLICATION NUMBER: US/09/213,053
 ; EARLIER FILING DATE: 1998-12-16
 ; EARLIER APPLICATION NUMBER: 9608242
 ; EARLIER FILING DATE: 1996-06-27
 ; EARLIER APPLICATION NUMBER: PCT/FR97/01115
 ; EARLIER FILING DATE: 1997-06-23
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 1394
 ; TYPE: PRT
 ; ORGANISM: Canine herpesvirus
 ; US-09-213-053-2

Query Match 4.0%; Score 109.5; DB 4; Length 1394;
 Best Local Similarity 20.4%; Pred. No. 0.087;
 Matches 114; Conservative 84; Mismatches 195; Indels 167; Gaps 26;
 OY 21 SVVSMNLFVALLACIYVGHLEENRWVNSITALLIGCTGVVILLSS-----GKSS 74
 DB 463 SLDCIGAGILTLALIIILQIL-----TSPVCSIIILNF-VLIPLSKTSISTSEKIS 515
 OY 75 HLIVFSEDLF-----FYLLPPIIFENAGFOVKKKQFVNPMITMLFGAIGTLISCS 125
 DB 516 SICRISQISIEVTIAFCWGMILNPI----- 542
 OY 126 IISFGAVKIFKHLIDIDLDGDIYLAIGAFRAIDSVCTLOVLSODETPLYLSLVFGGV- 184
 DB 543 -----AIRIILISLSP-----TICTIKI-----HIFYLITLNSGSH 577


```

1 STREET: 30 Rockefeller Plaza
2 CITY: New York
3 STATE: New York
4 COUNTRY: USA
5 ZIP: 10112
6
7 COMPUTER READABLE FORM:
8 MEDIUM TYPE: Floppy disk
9 COMPUTER: IBM PC compatible
10 OPERATING SYSTEM: PC-DOS/MS-DOS
11 SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
12
13 CURRENT APPLICATION DATA:
14 APPLICATION NUMBER: US/09/087,232A
15 FILING DATE: 28 May 1998
16 CLASSIFICATION: 435
17
18 PRIOR APPLICATION DATA:
19 APPLICATION NUMBER: 60/048,057
20 FILING DATE: 30 May 1997
21
22 ATTORNEY/AGENT INFORMATION:
23 NAME: KOLE, LISA B.
24
25 REGISTRATION NUMBER: 35,225
26 REFERENCE/DOCKET NUMBER: AP 31115
27
28 TELECOMMUNICATION INFORMATION:
29 TELEPHONE: (212) 408-2628
30 TELEFAX: (212) 765-2519
31
32 INFORMATION FOR SEQ ID NO: 13:
33 SEQUENCE CHARACTERISTICS:
34 LENGTH: 352 amino acids
35 TYPE: amino acid
36 TOPOLOGY: linear
37
38 MOLECULE TYPE: protein
39
40 US-09-087-232A-13

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Query Match	3.5%;	Score 97.5;	DB 4;	length 352;
Best Local Similarity	21.8%;	Pred. No. 0.17;		
Matches 66;	Conservative 53;	Mismatches 127;	Indels 57;	Gaps 14;

```

QY 173 PLKSLVFGEEVY--NDATSVYLFNAJOSFDMTSEDPKIGLHFIGNFLFLFSSSFFLAGI 231
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 34 PRLXSLVFIPEFVGMLVILLINCKRLAKSMTDI-----YLNLAISDDEFLLTV 83

QY 232 GLLCAY-----ITKKLYF--GRHSTDREVALMIMSYSTYMAELFYISGLT 277
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 84 PFMAYAAACMDPFGNTMQLTLGLYFIFFGEGIFELLITIDRYLAVVNA-VFALKARTV 142

QY 278 VEPFGIWSHTWNVNTESSR---VTRHSPATISFAVEFIFELVVGMDALDIEKRWK 334
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 143 TF--GVVTSVITVVAVAFASLPGLIFTRYSQKEGLHYTCSSH-FPY-----SOYQFWK 191

QY 335 NSOGHSVAVSSILLVGLI-LVGRAAFYRPLSEFLSLMAKKNSSDKISFRQOIT--ITMAGL 390
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 192 NFQRLKIYIGLIVLEPLVMYTCYSGILKTLRCRREKRRHRAVRILFIETIMVYFLFMA-- 249

QY 391 MRGAVSIALAYNKF-----YTSGHTSLHENAIMTST--VTVLESTVVEGLMTKPLIN 442
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 250 --PYNIVLLNTQEFFGLNNCSSNRIDQAMQVTEFTLGHTHCINPIIYAFVGEKFRN 306

QY 443 LLL 445
    | |
Db 307 YLL 309

```

RESULT 12
 US-08-661-105-14
 : Sequence 14, Application US/08661105
 : Patent No. 6256527
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: LITTMAN, DAN R.
 :
 : APPLICANT: DENG, HONGKUI
 :
 : APPLICANT: ELMEIER, WILFRIED
 :
 : APPLICANT: LANDAU, NATHANIEL R.
 :
 : APPLICANT: LIU, RONG
 :
 : TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
 : MACROPHAGE-TROPIC HIV, AND DIAGNOSTIC AND THERAPEUTIC

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 18, 2002, 12:24:11 ; Search time 31 Seconds
(without alignments)
3024.621 Million cell updates/sec

Title: US-09-830-123-2

Perfect score: 2768
Sequence: 1 MAFGLSLQLQNSDLFTSDHA.....FGGRGFVPVAGSPVQSPR 542

Scoring table:

BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeop:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	2768	100.0	542	10	O9FEB3
2	2726	98.5	542	10	O94IE0
3	2127.5	76.9	555	10	O9FZNO
4	2124.5	76.8	553	10	O94LX4
5	2103.5	76.0	540	10	O94LX5
6	2083.5	75.3	542	10	O9ARH6
7	2072	74.9	556	10	O94K25
8	2055.5	74.3	535	10	O9SXX8
9	2054.5	74.2	546	10	O9CAX6
10	2041	73.7	538	10	O9ZPK3
11	1953.5	70.6	555	10	O94LX3
12	1925.5	69.6	552	10	O9SQU0
13	1865.5	67.4	546	10	O94BM4
14	1819.5	65.7	534	10	O93YH2
15	1732.5	62.6	457	10	O04655
16	1600.5	57.8	529	10	O9FJ63

17	1107.5	40.0	295	10	O94BM3	O94bm3 triticum ae
18	620	22.4	561	5	O9XZH4	O9xzh4 drosophila
19	620	22.4	549	5	O9VPU1	O9vpj1 drosophila
20	591.5	21.4	703	5	O9XW14	O9xw14 caenorhabdi
21	585.5	21.2	725	4	O96T83	O96t83 homo sapien
22	576.5	20.8	687	5	O9U624	O9u624 drosophila
23	575.5	20.8	727	5	O9VM99	O9vm99 drosophila
24	563.5	20.4	616	4	O75827	O75827 homo sapien
25	556	20.1	569	3	O13726	O13726 schizosacch
26	552.5	20.0	629	5	O20944	O20944 caenorhabdi
27	526	19.0	153	10	O9LKH6	O9lkh6 mesembryant
28	523	18.9	140	10	O9LKH5	O9lkh5 mesembryant
29	512.5	18.5	531	10	O93YH1	O93yh1 lycopersico
30	483	17.4	518	5	O9VIF9	O9vif9 drosophila
31	474.5	17.1	1203	5	O9NGZ4	O9ngz4 drosophila
32	471	17.0	1179	5	O9NC00	O9ncq0 aedes aegypt
33	469.5	17.0	560	3	O9HEX3	O9hex3 pneumocysti
34	451	16.3	813	13	O9W6Q1	O9w6q1 amphiuma tr
35	448	16.2	437	4	O9Y507	O9y507 homo sapien
36	445.5	16.1	698	13	O9W724	O9w724 cyprinus ca
37	442	16.0	673	5	O23706	O23706 carctinus ma
38	442	16.0	779	13	O9W714	O9w714 platichthys
39	441.5	16.0	781	13	P70009	P70009 xenopus lae
40	425.5	15.4	555	4	O96EM2	O96em2 homo sapien
41	425.5	15.4	634	5	O9YZH0	O9yzh0 caenorhabdi
42	421	15.2	106	10	O9ATZ9	O9atz9 zea mays (m
43	419	15.1	478	5	O01995	O01995 caenorhabdi
44	410	14.8	411	4	O9Y2E8	O9y2e8 homo sapien
45	409.5	14.8	627	5	O09432	O09432 caenorhabdi

ALIGNMENTS

RESULT 1

ID O9FEB3 PRELIMINARY: PRT: 542 AA.
AC O9FEB3:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 19, Last annotation update)
DE NA+/H+ EXCHANGER (NA+/H+ EXCHANGER PROTEIN).
GN PURPLE OR INNHXL.
OS Phorbittis nil (Violet) (Japanese morning glory).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Convolvulaceae; Ipomoea.
OX NCBI_TaxID=35883;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KKZK-2; TISSUE=LEAF, AND FULLY COLORED FLOWER BUDS;
RX MEDLINE=20487008; PubMed=11034195.
RT Fukuda-Tanaka S., Inagaki Y., Yamaguchi T., Saito N., Iida S.;
RT "Colour-enhancing protein in blue petals.";
RL Nature 407:581-581(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=PR-R; TISSUE=LEAF;
RX MEDLINE=21276661; PubMed=11382810;
RA Yamaguchi T., Fukuda-Tanaka S., Inagaki Y., Saito N.,
RA Yonokura-Sakakibara K., Tanaka Y., Kusumi T., Iida S.;
RT "Genes Encoding the Vacuolar Na+/H+ Exchanger and Flower Coloration.";
RL Plant Cell Physiol. 42:451-461(2001).
DR EMBL: AB033990; BAB16381.1;
DR EMBL: AB033989; BAB16380.1;
DR EMBL: AB035062; BAB60899.1;
DR InterPro: IPR001179; FKBP_PPIase.
DR InterPro: IPR000676; Nah_Exchange.
DR Pfam: PF00999; Nah_Exchange; 1.
DR PRINTS: PR01084; NAHEXCHNG.
DR PROSITE: PS00453; FKBP_PPIASE_1; UNKNOWN_1.
SQ SEQUENCE 542 AA: 59973 MW: 4847FDE04A01A191 CRC64;

Query Match	100.0%	Score 2768;	DB 10;	Length 542;
Best Local Similarity	100.0%	Prod. No. 7.1e-204;		
Matches 542;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY 1	MAFGSSLLQNSDLEPTSPHASVSNKLEFVALLCACIVIGHLEENRWNESTITALITGIC	60		
DB 1	MAFGSSLLQNSDLEPTSPHASVSNKLEFVALLCACIVIGHLEENRWNESTITALITGIC	60		
QY 61	TGVVILLISGCKSSHLVFESEDFEYIYLLPIIFNAGFOVKKKQFVNMFTIMLFGAIGT	120		
DB 61	TGVVILLISGCKSSHLVFESEDFEYIYLLPIIFNAGFOVKKKQFVNMFTIMLFGAIGT	120		
QY 121	LISCSISFGGAKIFPKHLDIDFLDGDYIALGAIIPAADSVCTLOVLSODETPLLISLYE	180		
DB 121	LISCSISFGGAKIFPKHLDIDFLDGDYIALGAIIPAADSVCTLOVLSODETPLLISLYE	180		
QY 181	GGGVNDATSVYLFNAIOSFDMTSEDPKIGLHFGNPLYLFLSSTFLGVGIGLLCAYIIR	240		
DB 181	GGGVNDATSVYLFNAIOSFDMTSEDPKIGLHFGNPLYLFLSSTFLGVGIGLLCAYIIR	240		
QY 241	KLYPRHSRDREVALAMLMSTYSYIMAEFLYSGILTYPEFGCIWASHTHWNTSSRYT	300		
DB 241	KLYPRHSRDREVALAMLMSTYSYIMAEFLYSGILTYPEFGCIWASHTHWNTSSRYT	300		
QY 301	TRHSEATISFEVAETEIFLYVGMDALDIEKKKFKVKNQGLSVAVSSILVGLILVGRAEYF	360		
DB 301	TRHSEATISFEVAETEIFLYVGMDALDIEKKKFKVKNQGLSVAVSSILVGLILVGRAEYF	360		
QY 361	PLSFSLNIAKKKSSDKISIRQOIIITWAGLIMGAVSIALAYKKFTTSGTSHENAMIT	420		
DB 361	PLSFSLNIAKKKSSDKISIRQOIIITWAGLIMGAVSIALAYKKFTTSGTSHENAMIT	420		
QY 421	STVTVVLESTVYFGLMTKRLINLLPDKOMPQSGHSSMTTSEPPSKHFTVPLDNDPDS	480		
DB 421	STVTVVLESTVYFGLMTKRLINLLPDKOMPQSGHSSMTTSEPPSKHFTVPLDNDPDS	480		
QY 481	ESDMITGPEVAPRTALRMLLRTPTHTVHRKMKFDDSEFRKPYFGGRGYPYFVAGSPVEDS	540		
DB 481	ESDMITGPEVAPRTALRMLLRTPTHTVHRKMKFDDSEFRKPYFGGRGYPYFVAGSPVEDS	540		
QY 541	PR 542			
DB 541	PR 542			
RESULT 2				
Q94IE0	PRELIMINARY;	PRT;	542 AA.	
AC Q94IE0:				
DT 01-DEC-2001 (TREMBLrel. 19, Created)				
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)				
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)				
DE NA+/H+ EXCHANGER.				
GN ITNMH1.				
OS Ipomoea tricolor (Morning glory).				
OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;				
OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots;				
OC Asteridae: euasterids I; Solanales; Convolvulaceae; Ipomoea.				
OX NCBI_Taxid=89664;				
RP [1]				
RP SEQUENCE FROM N.A.				
RA MEDLINE=21276661; PubMed=11382810;				
RA Yamaguchi T., Fukuda-Tanaka S., Inagaki Y., Saito N.,				
RA Yonekura-Sakakibara K., Tanaka Y., Kusumi T., Iida S.,				
RT "Genes Encoding the Vacuolar Na+/H+ Exchanger and Flower Coloration,"				
RL Plant Cell Physiol. 42:451-461(2001).				
SD EMBL; AB054979; BAB60901.1; -				
SD SEQUENCE 542 AA; 60024 MW; 0C8381CFB78B239C CRC64;				

QY	1	MARGLSLDNDLPFSDHSAVSNMUEVALLCCAYUGHLTEENRVNVESTALLIGC	60
QY	1	MARGLSLDNDLPFSDHSAVSNMUEVALLCCAYUGHLTEENRVNVESTALLIGC <td>60</td>	60
Db	1	MARGLSLDNDLPFSDHSAVSNMUEVALLCCAYUGHLTEENRVNVESTALLIGC <td>60</td>	60
QY	61	TGVVILLISGKSSHLIVESEDLFFIYLLPPIINAGFOYKKOFENFMTIMLFGAIGT <td>12</td>	12
QY	121	LISCSIIISFCAVKEFKHLDIDPLDPEGDYLAIGAIPAATDSVCHLOYSODEPPLYSLVF <td>18</td>	18
Db	121	LISCSIIISFCAVKEFKHLDIDPLDPEGDYLAIGAIPAATDSVCHLOYSODEPPLYSLVF <td>18</td>	18
QY	181	GEGVVDNATSVVLEFNALIOSEDMTSFDPKIGLHFTGNFELYFLSTFELGVCIGLCAIYK <td>24</td>	24
Db	181	GEGVVDNATSVVLEFNALIOSEDMTSFDPKIGLHFTGNFELYFLSTFELGVCIGLCAIYK <td>24</td>	24
QY	241	KLYEGRHSTREVALMMLMSLYSTYIMAEFLYLSGILVFECGIYVSHYTHWNTBESSRVT <td>30</td>	30
Db	241	KLYEGRHSTREVALMMLMSLYSTYIMAEFLYLSGILVFECGIYVSHYTHWNTBESSRVT <td>30</td>	30
QY	301	TRHSFATLSVAETFFLVVGMDALDIEKKMFVKNOSGLSVANSTLYGLIIVGRAVVF <td>36</td>	36
Db	301	TRHSFATLSVAETFFLVVGMDALDIEKKMFVKNOSGLSVANSTLYGLIIVGRAVVF <td>36</td>	36
QY	361	PLSFSLNLAKNSSDISFROQIITIMWAGLMKGAVALANKEFTTSGHTSLHENAIMIT <td>42</td>	42
Db	361	PLSFSLNLAKNSSDISFROQIITIMWAGLMKGAVALANKEFTTSGHTSLHENAIMIT <td>42</td>	42
QY	421	STVTVVLFSTVTVVGLMTKPLINLLPRLPKOPSGHSSMTTSEBSPKHFVPLLDMDOPS <td>48</td>	48
Db	421	STVTVVLFSTVTVVGLMTKPLINLLPRLPKOPSGHSSMTTSEBSPKHFVPLLDMDOPS <td>48</td>	48
QY	481	ESDMITGEVAPRALMLRPTPTHVHRYWKRFPDSEFRMVFEGSGRFVFPVAGSPVEDS <td>54</td>	54
Db	481	ESDMITGEVAPRALMLRPTPTHVHRYWKRFPDSEFRMVFEGSGRFVFPVAGSPVEDS <td>54</td>	54
QY	541	PR 542 <td></td>	
Db	541	PR 542 <td></td>	
RESULT 3			
ID	Q9FZNO	PRELIMINARY:	PRT: 555 AA.
AC	Q9FZNO:		
DT	01-MAR-2001 (TREMBLrel, 16, Created)		
DT	01-MAR-2001 (TREMBLrel, 16, Last sequence update)		
DT	01-DEC-2001 (TREMBLrel, 19, Last annotation update)		
DE	NA/H ANTIPORTER NHX1.		
GN	AGNHX1.		
OS	Atirplex gmelini.		
OC	Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;		
OC	SpERMATOPHYTES: Magnoliophyta: eudicotyledons: core eudicots;		
OC	Caryophyllales: Caryophyllales; Chenopodiaceae: Atirplex.		
OX	NCBI_TaxID=118074;		
RP	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=21330247; PubMed=11437248;		
RA	Hamada A., Shono M., Xia T., Ohta M., Hayashi Y., Tanaka A.,		
RT	Hayakawa T.;		
RT	"Isolation and characterization of a Na ⁺ /H ⁺ antiporter gene from thea		
RL	halophyte Atirplex gmelini.";		
DR	Plant Mol. Biol. 46:35-42(2001).		
DR	EMBL; AB038492; BAB11940.1; -;		
DR	InterPro; IPR001179; KFBP_PPIase.		
DR	InterPro; IPR000676; NaH_Exchange.		
DR	Pfam; PF00999; Na_H_Exchange; 1.		
DR	PRINTS; PRO1084; NAHEXCHNGR.		
DR	PROSITE; PS00453; KFBP_PPIase_1; UNKNOWN_1.		
SO	SEQUENCE 555 AA; 61504 MW; ACD5ED45FF3D398A CRC64;		
Query Match	76.9%;	Score 2127.5;	DB 10; Length 555;
Best Local Similarity	76.6%;	Pred. No. 7.8e-155;	

[illegible]

OY	60	CNGVYLLLSGKSSHLVFSQDLEFYLPRPIINNAFOYKKQFPVNEMTIMFGAIG	119
Db	61	CTGVYILLISGKNSHLIVFSEDFEYLLPPIIFMAFOYKKKSFFENSTIMFGAVG	120
OY	120	TLTSGSIISFGAVKLFKMLIDFLDFCGYLAIGAFAATDSVCTLQVYSOQETPLTSLV	179
Db	121	TLTSLIISAGAIIGAFKKMDIGHLETGYLAIGAFAATDSVCTLQVNOGETPLTSLV	180
OY	180	FEGGVNDAATSVYLENAIOSFDMTSFDPRIGLHFIQNFLLYPLSSTELGVCIGLCAYII	239
Db	181	FEGGVNDATSVYLENAVOINFDSHSITGKALLOLLGNFLYFASSTETGVAVGILLSAFII	240
OY	240	KKLTYGRHSTDDEVALLMIMSYLSYIMAELEPLSGILVFPCGIYMSHYTHANNTESRV	299
Db	241	KKLTYGRHSTDDEVAIMIMAMLSLMLELYLSGILTVFCGIYMSHYTHANTESSRV	300
OY	300	TTRHSFATLSFYAETFEFLYVGMDALDIKKMFVKNSOGLSVAYSILVGLILVGRAFV	359
Db	301	TTRKHTEATLSFYAETFEFLYVGMDALDIKKMFVS DSPGSITIKVSYILLGLVLVGRCAFV	360
OY	360	PRLSPFLSNLAKKNSSDKISFRQIITIMWAGLMRGAVSIALYNNFTTSGHTSLKENAMI	419
Db	361	PRLSPFLSNLTKKNPBKDISFNQOVYIMWAGLMRGAVSIALYNFTTGHQTOLKANAMI	420
OY	420	TSTVTYVLESTYVFEGLMKTPRLINLIPRHKOMPSSGMTSESPPKHFPTLLDNOPD	479
Db	421	TSTITYVLESTYVFEGLMKTPRLILLRP SQNH ---- IMISSBPMTPKSFVLPDLBSTOD	476
OY	480	SSEDMITGEVARPALPMLRTPTHTVHYRWKRKFDSFMRFVPGRGEPVAGSVE	538
Db	477	SEADL--GRHVPRPHSLRMLLSTPSHTVHYWRKFDNAFMRPVPGRGEPVPVGSPE	533
 RESULT 5 Q94IX5 PRELIMITARY; PRT: 540 AA.			
AC	094LX5:	01-DEC-2001 (TREMBREL, 19, Created)	
DT	01-DEC-2001 (TREMBREL, 19,	Last sequence update)	
DT	01-DEC-2001 (TREMBREL, 19,	Last annotation update)	
DE	NA H-ANTIORTOR.		
GN	PHURPLE.		
OS	Petunia hybrida (Petunia).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		
OC	Asteridae; euasterids I; Solanales; Solanaceae; Petunia.		
NCBI_TaxId=4102;	[1]		
RN	SEQUENCE FROM N.A.		
RA	Iida S., Kusumi T., Yonekura-Sakakibara K., Tanaka Y.;		
RT	"Plant Na-H antiporter.";		
RL	Submitted (NOV-2000) to the EMBL/GenBank/DDIJ databases.		
DR	EMBL; AB051817; BAB56105.1; -.		
SQ	SEQUENCE 540 AA; 59510 MW; BCE2740B275EB96A CRC64;		
 Query Match 76.0%; Score 2103.5; DB 10; Length 540; Best Local Similarity 76.4%; Pred. No. 5.2e-153; Matches 412; Conservative 51; Mismatches 69; Indels 7; Gaps 3;			
OY	1	MAFGSLILOUSD-LFTSDHASVSMNLFWALLCACATIVGHLLENRMVNESITALITGL	59
Db	1	MAFDGCTLLGNVDRLSTSDHOSVSNLFWALLCACIVIGHILEENRMNESITALYTGS	60
OY	60	CTGVYILLISGKSSHLVFSQDLEFYLPRPIIFNAGFOYKKKOFVNMFTMLEGAIG	119
Db	61	CTGIYILLISGGKNSHILVFSQDLEFYLPRPIIFNAGFOYKKKSFFRNSTIMLGALG	120
OY	120	TLTSCSIISFGAVKLFKMLIDFLDFCGYLAIGAFAATDSVCTLQVNOGETPLTSLV	179
Db	121	TLTSLIISAGAIIGAFKKMDIGHLETGYLAIGAFAATDSVCTLQVNOGETPLTSLV	180
OY	180	FEGGVNDAATSVYLENAIOSFDMTSFDPRIGLHFIQNFLLYPLSSTELGVCIGLCAYII	239
Db	181	FEGGVNDATSVYLENAVOINFDSHSITGKALLOLLGNFLYFASSTETGVAVGILLSAFII	240
OY	240	KKLTYGRHSTDDEVALLMIMSYLSYIMAELEPLSGILVFPCGIYMSHYTHANNTESRV	299
Db	241	KKLTYGRHSTDDEVAIMIMAMLSLMLELYLSGILTVFCGIYMSHYTHANTESSRV	300
OY	300	TTRHSFATLSFYAETFEFLYVGMDALDIKKMFVKNSOGLSVAYSILVGLILVGRAFV	359
Db	301	TTRKHTEATLSFYAETFEFLYVGMDALDIKKMFVS DSPGSITIKVSYILLGLVLVGRCAFV	360
OY	360	PRLSPFLSNLAKKNSSDKISFRQIITIMWAGLMRGAVSIALYNNFTTSGHTSLKENAMI	419
Db	361	PRLSPFLSNLTKKNPBKDISFNQOVYIMWAGLMRGAVSIALYNFTTGHQTOLKANAMI	420
OY	420	TSTVTYVLESTYVFEGLMKTPRLINLIPRHKOMPSSGMTSESPPKHFPTLLDNOPD	479
Db	421	TSTITYVLESTYVFEGLMKTPRLILLRP SQNH ---- IMISSBPMTPKSFVLPDLBSTOD	476
OY	480	SSEDMITGEVARPALPMLRTPTHTVHYRWKRKFDSFMRFVPGRGEPVAGSVE	538
Db	477	SEADL--GRHVPRPHSLRMLLSTPSHTVHYWRKFDNAFMRPVPGRGEPVPVGSPE	533
 RESULT 5 Q94IX5 PRELIMITARY; PRT: 540 AA.			
AC	094LX5:	01-DEC-2001 (TREMBREL, 19, Created)	
DT	01-DEC-2001 (TREMBREL, 19,	Last sequence update)	
DT	01-DEC-2001 (TREMBREL, 19,	Last annotation update)	
DE	NA H-ANTIORTOR.		
GN	PHURPLE.		
OS	Petunia hybrida (Petunia).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		
OC	Asteridae; euasterids I; Solanales; Solanaceae; Petunia.		
NCBI_TaxId=4102;	[1]		
RN	SEQUENCE FROM N.A.		
RA	Iida S., Kusumi T., Yonekura-Sakakibara K., Tanaka Y.;		
RT	"Plant Na-H antiporter.";		
RL	Submitted (NOV-2000) to the EMBL/GenBank/DDIJ databases.		
DR	EMBL; AB051817; BAB56105.1; -.		
SQ	SEQUENCE 540 AA; 59510 MW; BCE2740B275EB96A CRC64;		
 Query Match 76.0%; Score 2103.5; DB 10; Length 540; Best Local Similarity 76.4%; Pred. No. 5.2e-153; Matches 412; Conservative 51; Mismatches 69; Indels 7; Gaps 3;			
OY	1	MAFGSLILOUSD-LFTSDHASVSMNLFWALLCACATIVGHLLENRMVNESITALITGL	59
Db	1	MAFDGCTLLGNVDRLSTSDHOSVSNLFWALLCACIVIGHILEENRMNESITALYTGS	60
OY	60	CTGVYILLISGKSSHLVFSQDLEFYLPRPIIFNAGFOYKKKOFVNMFTMLEGAIG	119
Db	61	CTGIYILLISGGKNSHILVFSQDLEFYLPRPIIFNAGFOYKKKSFFRNSTIMLGALG	120
OY	120	TLTSCSIISFGAVKLFKMLIDFLDFCGYLAIGAFAATDSVCTLQVNOGETPLTSLV	179
Db	121	TLTSLIISAGAIIGAFKKMDIGHLETGYLAIGAFAATDSVCTLQVNOGETPLTSLV	180
OY	180	FEGGVNDAATSVYLENAIOSFDMTSFDPRIGLHFIQNFLLYPLSSTELGVCIGLCAYII	239
Db	181	FEGGV	

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Db 181 FGEVYNDATSVLFNMIQNFDSLHIDTGKAMELVGNFLYFASSTALGVAAGLSAYII 240
QY 240 KKLFGHSTDEVALMMKLSYIYMAELFYLSGILTFPGCGIYMSHYTHNTSSRV 299
Db 241 KKLFGHSTDEVALIMLAVLSYMAELFYLSAILTFPGSGIYMSHYTHNTSSRV 300
QY 300 TTRHSFATLSVAEFIFLYGMDALDEKMKFVKNSOGLSVAVSSILVGLIYGRAAFV 359
Db 301 TTKHFTALSLIAELFFLYGMDALDEKMKFVSDSGISVOYSSILGLIYVGRAPV 360
QY 360 FPLSLMIAKNSDKISFRQOIIIMWAGLMRGAVSIALAYNKFTTSGHTSLHENAIMI 419
Db 361 FPLSLMIAKNSDKISFRQOIIIMWAGLMRGAVSIALAYNKFTTSGHTSLHENAIMI 420
QY 420 TSTYVYVLFSTVYVGLMKRPLINLLPPHKOMPSGHSMTSESPSKHFTVPLLDNDP 479
Db 421 TSTYVYVLFSTVYVGLMKRPLIRLLPSKHL---SMTISEPTTPSPFTVPLLDNDP 476
QY 480 SESDMITPEVAPRTALMLRTPTHTVHYRWKRFDDSFMRPFVGRGFVFAVGSPE 538
Db 477 SEADL--ERHVPKPSHMLSTSHYHYWKRFDAFMKPFVGRGFVFAVGSPTD 533

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RESULT 6

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Q9ARH6 PRELIMINARY; PRT; 542 AA.
ID 09ARH6.
AC 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE SODIUM/PROTON EXCHANGER.
OS Citrus paradisi (Grapefruit).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustosids II; Sapindales; Rutaceae; Citrus.
OX NCBI_TaxID=37656;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PEEL;
RA Porat R., Lurie S., Poyanecello D.;
RT "A heat treatment induced the transcription of a sodium proton
RT exchanger gene in grapefruit peel tissue.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY028416; AAK27314.2; -.
SQ SEQUENCE 542 AA; 59836 MW; 1A8525F2C5FAEE2C CRC64;

```

Query Match 75.3%; Score 2083.5; DB 10; Length 542;

Best Local Similarity 75.4%; Pred. No. 1.8e-151;

Matches 407; Conservative 61; Mismatches 65; Indels 7; Gaps 5;

```

QY 5 TSSILQNSDLF-TSDHASVSNMFLVALLCACIYVGHLLLENRWVNESITALLIGLCTGV 63
Db 5 TSSVVRKILQWNTSDHNSVSNITFVALPCASIVYGHLLSEKRMNESITALLIGVCAGV 64
QY 64 VILLISGKSSHLVFESEDLFFIYLLPPIFNAGFQVKKQFVNFMTIMFGAIGTILS 123
Db 65 ILLLTGKGSSHLVFESEDLFFIYLLPPIFNAGFQVKKQFNFMTIMFGAIGTILS 124
QY 124 CSITFGAVKIRKHLIDIFLDPGDYLAIGATFAATDSVCTILOYSDQETPLISLVBE 183
Db 125 CIIISLGYIOFKKLDIGTLDIGDYLAIGATFAATDSVCTILOYSDQETPLISLVBE 184
QY 184 VYNDATSVLFNAIOSFMTSPDKIGLHFIQNFYLLFSLSTFGLVGIGLCAVYIKLY 243
Db 185 VYNDATSVLFNAIOSFMTSPDKIGLHFIQNFYLLFSLSTFGLVGIGLCAVYIKLY 244
QY 244 FGRHSITDEVALMMKLSYIYMAELFYLSGILTFPGCGIYMSHYTHNTSSRVTRH 303
Db 245 FGRHSITDEVALMMKLSYIYMAELFYLSGILTFPGCGIYMSHYTHNTSSRVTRH 304
QY 304 SFATISFAETIFLYVGDALDIKMKFVKNSSGLSAVSSILVGLIYGRAAFVPLS 363
Db 305 TFAITSFVAEITFLYVGDALDIKMKFVKNSSGLSAVSSILVGLIYGRAAFVPLS 364

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QY 364 FLNLAKNSDKISFRQOIIIMWAGLMRGAVSIALAYNKFTTSGHTSLHENAIMITSV 423
Db 365 FLNLAKNSDKISFRQOIIIMWAGLMRGAVSIALAYNKFTTSGHTSLHENAIMITSV 424
QY 424 TVVLFSTVYVGLMKRPLINLLPPHKOMPSGHSMTSESPSKHFTVPLLDNDPDES 482
Db 425 TVVLFSTVYVGLMKRPLIRLL-PPKHTTNH---TLSPSTPKSLSOPFLMEGODSYA 480
QY 483 DMITGEVAPRTALMLRTPTHTVHYRWKRFDDSFMRPFVGRGFVFAVGSPEOSPR 542
Db 481 DLV-GPTVPPGSLRALTTPTHTVHYRWKRFDDSFMRPFVGRGFVFAVGSPTERSVR 539

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RESULT 7

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Q9AK25 PRELIMINARY; PRT; 556 AA.
ID 09AK25.
AC 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE NA+/H+ ANTIporter.
OS Suaeda maritima subsp. salsa.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllales; Chenopodiaceae; Suaeda.
OX NCBI_TaxID=126914;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang H., Zhang Q., Ma X.;
RT "Na+/H+ antiporter in Suaeda salsa.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF370358; AAK53432.1; -.
SQ SEQUENCE 556 AA; 61672 MW; DDE6AB696647D48E CRC64;

```

Query Match 74.9%; Score 2072; DB 10; Length 556;

Best Local Similarity 75.6%; Pred. No. 1.4e-150;

Matches 402; Conservative 58; Mismatches 62; Indels 10; Gaps 2;

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QY 16 TSDHASVSNMFLVALLCACIYVGHLLLENRWVNESITALLIGLCTGVYLLISGKSSH 75
Db 18 TSDHASVSNMFLVALRCGCIYVGHLLLENRWVNESITALLIGLCTGVYLLISGKSSH 77
QY 76 LVFESEDLFFIYLLPPIFNAGFQVKKQFVNFMTIMFGAIGTILSISFGAVKIF 135
Db 78 LVFESEDLFFIYLLPPIFNAGFQVKKQFNFMTIMFGAIGTILSISFGAVKIF 137
QY 136 KHLIDIFLDPGDYLAIGATFAATDSVCTILOYSDQETPLISLVBEQVYNDATSVLFN 195
Db 138 QKMDIGSLIEGLDYLGAIFAAATDSVCTILOYSDQETPLISLVBEQVYNDATSVLFN 197
QY 196 AIOSEDMTPEVAPRTALMLRTPTHTVHYRWKRFDDSFMRPFVGRGFVFAVGSPE 255
Db 198 AIOSEDMTPEVAPRTALMLRTPTHTVHYRWKRFDDSFMRPFVGRGFVFAVGSPE 257
QY 256 MMLMSYLSYIMAEFLYLSGILTFPGCGIYMSHYTHNTSSRVTRHFAITSEVAEFP 315
Db 258 MMLMSYLSYIMAEFLYLSGILTFPGCGIYMSHYTHNTSSRVTRHFAITSEVAEFP 317
QY 316 IFLYVGDALDIKMKFVKNSSGLSAVSSILVGLIYGRAAFVPLSLNKAANSND 375
Db 318 IFLYVGDALDIKMKFVKNSSGLSAVSSILVGLIYGRAAFVPLSLNKAANSND 377
QY 376 KISFRQOIIIMWAGLMRGAVSIALAYNKFTTSGHTSLHENAIMITSVYVLFSTVYVGL 435
Db 378 KISFRQOIIIMWAGLMRGAVSIALAYNKFTTSGHTSLHENAIMITSVYVLFSTVYVGL 437
QY 436 MTKRPLINLLPPHKOMPSGHSMTSESPSKHFTVPLLDNDPDESMDITGE----- 489
Db 438 LTKRPLIFMLPQPKHFT---SASTVSDLGSPKSFSLPLEDRDSDADLGDDEEAYPRG 494
QY 490 -VAPRTALMLRTPTHTVHYRWKRFDDSFMRPFVGRGFVFAVGSPEOS 540

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Db 495 T1ARPTSLRMLNLAPTHVHHWRREDYFMRPFVGGRGFPVPGSPTEQS 546

RESULT 8
ID 09SXJ8 PRELIMINARY; PRT: 535 AA.
AC 09SXJ8;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE OSNXX1 PROTEIN.
GN OSNXX1.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eubacteriobacteriota; Oryzaeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RX MEDLINE=99326147; PubMed=10395929;
RA Fukuda A., Nakamura A., Tanaka Y.;
RT "Molecular cloning and expression of the Na⁺/H⁺ exchanger gene in
Oryza sativa.",
RL Biochim. Biophys. Acta 1446:149-155(1999).
DR EMBL; AB021876; BAA83337.1; -;
DR InterPro; IPR000676; NaH_Exchng.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR PRINTS; PR01084; NAHEXCHNGR.
SQ SEQUENCE 535 AA; 59070 MW; 6BCADBD29B131976 CRC64;

Query Match 74.3%; Score 2055.5; DB 10; Length 535;
Best Local Similarity 76.4%; Pred. No. 2.4e-149;
Matches 401; Conservative 49; Mismatches 66; Indels 9; Gaps 3;

QY 16 TSDHASVSNMFLVALLACACIVLGHLEENRWNESTLIIIGLCTGVVILLSGKSSH 75
DB 16 TSDYASVSNMFLVALLACACIVLGHLEENRWNESTLIIIGLCTGVVILLMTGKSSH 75
QY 76 LVFSEDFEFTYLLPPIFNAGFOVKKOFPNMTIMLFGAIGTLISISFGAVKFE 135
DB 76 LVFSEDFEFTYLLPPIFNAGFOVKKOFPNMTIMLFGAIGTLISISFGAVKFE 135
QY 136 KHLIDFDFGDLAIGAIFAATDSVCTLOVLSODETPLLSLVFGGVNDATSVLFN 195
DB 136 KHLIDFDFGDLAIGAIFAATDSVCTLOVLSODETPLLSLVFGGVNDATSVLFN 195
QY 136 SRNNIGTLDVGDFLAIGAIFSATDSVCTLOVLSODETPLLSLVFGGVNDATSVLFN 195
DB 136 SRNNIGTLDVGDFLAIGAIFSATDSVCTLOVLSODETPLLSLVFGGVNDATSVLFN 195
QY 196 AIOSFDMTSFDPKIGLHFGNLFYLSSTFGVGGIGLLCAITIKKLYGRKSTREVAL 255
DB 196 AIOSFDMTSFDPKIGLHFGNLFYLSSTFGVGGIGLLCAITIKKLYGRKSTREVAL 255
QY 256 MMLMSYLSYMAELFYLSGILTVFPGCIYMSHYTMHNVTSESSRVTRHSFATLFEVAF 315
DB 256 MMLMSYLSYMAELFYLSGILTVFPGCIYMSHYTMHNVTSESSRVTRHSFATLFEVAF 315
QY 316 IFLYGMADLDEKMEFYKANSOGSLVAVSSILVGLLVGAAVFPPLSLMLAKNSSD 375
DB 316 IFLYGMADLDEKMEFYKANSOGSLVAVSSILVGLLVGAAVFPPLSLMLAKNSSD 375
QY 376 KISFROOIIIMAGLARGVAVSTALVYNNKFTTSGHSLHENAIMITSYTVLFSTVVG 435
DB 376 KISFROOIIIMAGLARGVAVSTALVYNNKFTTSGHSLHENAIMITSYTVLFSTVVG 435
QY 436 MKRPLINLLPRLPHKQMPSCSHSMSTSESSPKHFTVPLDNDOPDESDMITGPEVARPTA 495
DB 436 MKRPLINLLPRLPHKQMPSCSHSMSTSESSPKHFTVPLDNDOPDESDMITGPEVARPTA 495
QY 496 LKMLLTPRHVTHRYKRWKAKDDSFMRPVGGRGFPVPGSPTEQS 540
DB 496 LKMLLTPRHVTHRYKRWKAKDDSFMRPVGGRGFPVPGSPTEQS 540
QY 540 LKMLLTPRHVTHRYKRWKAKDDSFMRPVGGRGFPVPGSPTEQS 540
DB 540 LKMLLTPRHVTHRYKRWKAKDDSFMRPVGGRGFPVPGSPTEQS 540

RESULT 9

09CAG6
ID 09CAG6 PRELIMINARY; PRT: 546 AA.

AC 09CAG6;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE PUTATIVE SODIUM PROTON EXCHANGER.
GN T9J14.2.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=21016720; PubMed=11130713;
RA Salanoubat M., Lemcke K., Rieger M., Ansoorge W., Unseld M.,
FArtmann B., Valle G., Bloeker H., Perez-Alonso M., Obermayer B.,
RA Delseny M., Boutry M., Grivell L.A., Mache R., Putgdomenech P.,
RA De Simone V., Choisme N., Artiguenave F., Robert C., Brotlier P.,
RA Wincker P., Catolico L., Weissenbach J., Saurin W., Queller F.,
RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA Wümbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,
RA Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Verzi A., D'Angelo M., Pallavicini A., Toppo S., Simonati B.,
RA Corrad A., Hornischer K., Kauer G., Loehmet T.-H., Nordstiek G.,
RA Reichelt J., Scharte M., Schoen O., Barges M., Terol J., Climent J.,
RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
RA Cooke R., Laudie M., Berger-Liauro C., Purnelle B., Masny D.,
RA Monfort A., Argillon A., Flores M., Liguori R., Vitale D.,
RA Mannhaupt G., Haase D., Schoof H., Rued S., Zaccaria P., Mewes H.-W.,
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA Rooney T., Rizzo M., Wals A., Ulteback T., Fujii C.Y., Shea T.P.,
RA Greasy T.H., Haas B., Malt R., Wu D., Peterson J., Van Aken S.,
RA Pal G., Miltischer J., Sellers P., Gill J.E., Feldblyum T.V.,
RA Preuss D., Lin X., Nieman W.C., Salzberg S.L., White O., Venter J.C.,
RA Fraser C.M., Kaneo T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Sasamoto S., Kimura T., Itoesawa K., Kawashima K., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
RA Watanabe A., Yamada M., Yasuda M., Tabata S.;
RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
thaliana.",
RL Nature 408:820-822(2000).
DR EMBL; AC009465; AAG51408.1; -;
DR InterPro; IPR001179; FKBP_P1ase.
DR InterPro; IPR000676; NaH_Exchng.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR PRINTS; PR01084; NAHEXCHNGR.
DR PROSITE; PS00453; FKBP_P1ase_1; UNKNOWN_1.
SQ SEQUENCE 546 AA; 60522 MW; BEA270D0446360B CRC64;

Query Match 74.2%; Score 2054.5; DB 10; Length 546;
Best Local Similarity 75.4%; Pred. No. 3e-149;
Matches 401; Conservative 56; Mismatches 60; Indels 15; Gaps 4;

QY 16 TSDHASVSNMFLVALLACACIVLGHLEENRWNESTLIIIGLCTGVVILLSGKSSH 75
DB 16 TSDHASVSNMFLVALLACACIVLGHLEENRWNESTLIIIGLCTGVVILLSGKSSH 75
QY 76 LVFSEDFEFTYLLPPIFNAGFOVKKOFPNMTIMLFGAIGTLISISFGAVKFE 135
DB 76 LVFSEDFEFTYLLPPIFNAGFOVKKOFPNMTIMLFGAIGTLISISFGAVKFE 135
QY 136 KHLIDFDFGDLAIGAIFAATDSVCTLOVLSODETPLLSLVFGGVNDATSVLFN 195
DB 136 KHLIDFDFGDLAIGAIFAATDSVCTLOVLSODETPLLSLVFGGVNDATSVLFN 195
QY 196 AIOSFDMTSFDPKIGLHFGNLFYLSSTFGVGGIGLLCAITIKKLYGRKSTREVAL 255
DB 196 AIOSFDMTSFDPKIGLHFGNLFYLSSTFGVGGIGLLCAITIKKLYGRKSTREVAL 255
QY 256 MMLMSYLSYMAELFYLSGILTVFPGCIYMSHYTMHNVTSESSRVTRHSFATLFEVAF 315
DB 256 MMLMSYLSYMAELFYLSGILTVFPGCIYMSHYTMHNVTSESSRVTRHSFATLFEVAF 315
QY 316 IFLYGMADLDEKMEFYKANSOGSLVAVSSILVGLLVGAAVFPPLSLMLAKNSSD 375
DB 316 IFLYGMADLDEKMEFYKANSOGSLVAVSSILVGLLVGAAVFPPLSLMLAKNSSD 375
QY 376 KISFROOIIIMAGLARGVAVSTALVYNNKFTTSGHSLHENAIMITSYTVLFSTVVG 435
DB 376 KISFROOIIIMAGLARGVAVSTALVYNNKFTTSGHSLHENAIMITSYTVLFSTVVG 435
QY 436 MKRPLINLLPRLPHKQMPSCSHSMSTSESSPKHFTVPLDNDOPDESDMITGPEVARPTA 495
DB 436 MKRPLINLLPRLPHKQMPSCSHSMSTSESSPKHFTVPLDNDOPDESDMITGPEVARPTA 495
QY 496 LKMLLTPRHVTHRYKRWKAKDDSFMRPVGGRGFPVPGSPTEQS 540
DB 496 LKMLLTPRHVTHRYKRWKAKDDSFMRPVGGRGFPVPGSPTEQS 540
QY 540 LKMLLTPRHVTHRYKRWKAKDDSFMRPVGGRGFPVPGSPTEQS 540
DB 540 LKMLLTPRHVTHRYKRWKAKDDSFMRPVGGRGFPVPGSPTEQS 540


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OY      IKLLYEGHSHDREVALMLMLMSYLSYMAELFYLSGLLYVEFGCIYMSHYTMHWNTESSR 2387
OY      229  IKLLYEGHSHDREVALMLMLMSYLSYMAELFYLSGLLYVEFGCIYMSHYTMHWNTESSR 2388
Db      241  IKLLYEGHSHDREVALMLMLMSYLSYMAELFYLSGLLYVEFGCIYMSHYTMHWNTESSR 3000
OY      299  VTRHSHFATLSFVAETEFLEYVGDADLDIEKMFVKNSOGLSVSSILYGLILYGRAAF 3588
Db      301  VTRKTHFATLSFVAETEFLEYVGDADLDIEKMRVSSMTMSAANVSLTGLVILSSAAF 3600
OY      359  VEPFLSENLAKKNSDKISFRQOIIITWAGLIMGANSIALANVKFTTSGHSLSHENAIM 418
Db      361  VEPFLSENLAKKNSDKLEKISLRQOIIITWAGLIMGAVSMALAKQFIREGLYVERENALF 4200
OY      419  ITSITVVLSESTVVFGLMTKPLINLLPRHKNOMSGHSSMTTSEPPSKHFTVBLDNCP 478
Db      421  ITSITVVLSESTVVFGLMTKPLINLLIPRXLNS-----VSSPELPRNSITITPLLGESQ 475
OY      479  DSESMIT-----GPEVAPALMLMLRTPHRTVHYRKWKRFDDSFMRPVGGGRFVP 530
Db      476  DSVAMELEIRICQTSOGGEPAPARPSLSMLLKPLPHITVHYWKRFDDNFMRPVGGGRFVP 535
OY      531  FVAGSPVEOSPR 542
Db      536  YPGSPTRERSVR 547

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RESULT 12	ID	Q95Q00	PRELIMINARY;	PRT;	552 AA.
AC	Q95Q00;				
DT	01-MAY-2000 (TREMBLrel. 13, Created)				
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)				
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)				
DE	PURINATIVE SODIUM PROTON EXCHANGER.				
GN	F24P17.16.				
OS	Arabidopsis thaliana (Mouse-ear cress).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; eudicotyledons: core eudicots; Rosidae;				
OC	eucosids II; Brassicales; Brassicaceae; Arabidopsids.				
NC	NCBI_TaxId=3702;				
LN	[1]				
RP	'SEQUENCE FROM N.A.				
RC	STRAIN=CV. COLUMBIA;				
RA	Lin H., Kaul S., Town C.D., Benito M., Greasy T.H., Haas B.,				
RA	Romling G., Koo H., Fujii C.Y., Utteback T.R., Barnstead M.E.,				
RA	Bowman C.L., White O., Nierman W.C., Fraser C.M.;				
RT	'Arabidopsis thaliana chromosome II BAC F24P17 genomic sequence.';				
RL	Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AC011623; AAF08577.1; -				
DR	InterPro; IPR001179; FKBP_P1ase.				
DR	InterPro; IPR000676; NaH_Exchange.				
DR	Pfam; PF00999; Na_H_Exchange; 1.				
DR	PRINTS; PS01084; NAHEXCHNR.				
DR	PROSITE; PS00453; FKBP_P1ase_1. UNKNOWN_1.				
SO	SEQUENCE 552 AA; 61135 MW; FB4317DBA874FCE9 CRC64;				

Query Match	69.6%;	Score 1925.5;	DB 10;	Length 552;
Best Local Similarity	70.4%;	Pred. No. 2.2e-139;		
Matches 381;	Conservative	59;	Mismatches 94;	Indels 7;
				Gaps 3;

QY	1	MAFBLSSLLONSD-LEPM	SDHASYVSNMLFVALL	CACIVLGHLEENRWNE	ITALIIGL	59
Db	1	MVGLSTMLKERTKTEAL	EFASDASHVSNMLFVALL	CACIVLGHLEETRWNE	ITALIIGS	60
QY	60	CTGVVILLISGGKSSHL	LVSEDFEFLYLLPPIIF	NANGFQVKKKOPFVN	MTIMLGATG	119
Db	61	CTGVVILLISGGKSSRL	LVSEDFEFLYLLPPIIF	NANGFQVKKKOPFVN	MTIMLGATG	120
QY	120	TLISCSIIISFGAVKIF	EKKHLIDFLDFGDIY	LAIGAFATSVCTLOYL	SODETPILYSIV	179
Db	121	TLISFVLIISFGAKHLE	EKKMNIIGDITLADY	LAIGAFATSVCTLOYL	SODETPILYSIV	180
QY	180	FGEYVVDATSVYLFNA	IQSFDMKTSDEPKIG	LHFIGNFLVLLSSYFL	GVGIGLLCAYII	239

Db	181	FEQGVVNATSVYLEFNALQOREDLITJNSALAEFAGNFYLFILSTLALVAGALLSAFVI	240b
Qy	240	KLYFGGRSTDEVALMMLMSTLSTIMALELYLSGILTYFPCGJYMSHYTMHNTDESRV	299b
Db	241	KLYLGRHSTDEVALMMLLAVLSMALIELHLSLSILTYFPCGJYMSHYTMHNTDCKSV	300b
Qy	300	TTRHSEFATLSEFAETFEFLUYGMALDIEKKRPKNSOGLSVAASITLYGILYGRAFV	359b
Db	301	TKKHFFAAMSPLAEFFIFLYGMALDIEKKDYVRNPSGOSIGVSSILGLITLIGRAFV	360b
Qy	360	PLFSLSLNLAKKNSDKTSFPOQIIIMWAGLRCGAVSIALAYNFTTSGHTSLHENAIMI	419b
Db	361	PLFSLSLNLTSSPDEKIDLKQVYIMWAGLRCGAVSIALAYNFTTSGHTKVLGNAMI	420b
Qy	420	TSTVAVVLESPVVEGLMKRPLINLLLRPHKQMPGSHSMTTSESSSKHNTVRLDNDOPD	479b
Db	421	TSTVAVVLESTVVEGLMKRPLVKNHLOPSSKOSTTALQITLRSSEFNDRLNHEPLSTQOG	480b
Qy	480	SESDMITPREVAPRALMLRLTPTUHNHQRKRFDDSFMRPVYGGRGFRVFAAGSVEQ	539b
Db	481	SEYD----PE--QHNSFEMFKPSSRAIHNHNRKFDNANVRIRITGGNGVSPVYVPGSPLEN	534b
Qy	540	S 540	
Db	535	S 535	

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RESULT 13
O94BM4
ID O94BM4 PRELIMINARY; PRT; 546 AA.
AC O94BM4;
DI 01-DEC-2001 (TrEMBLrel. 19, Created)
DI 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DI 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Na+/H+ ANTIporter.
GN NHX1.
OS Trilicium aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Triticum.
CC NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RA Wang Z., Zhang J., Chen S.;
RT "Isolation and characterization of two Na+/H+ antiport genes from
RT wheat.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY040245; AAK76737.1; -.
SQ SEQUENCE 546 AA; 59704 MW; 45EB1BCAB73E295C6 CRC64;

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Query Match	67.48;	Score 1865.5;	DB 10;	Length 546;
Best Local Similarity	68.28;	Pred. No. 8.7e-135;		
Matches 369;	Conservative 67;	Mismatches 92;	Indels 13;	Gaps 4;

QY	1	MAFGJSSJ-LONSDJFSDHSAVSMMJFVALLACALYGLHLEENRMVNESTIALJGL	59
Db	1	MGLDGLALALKYRTGSLAASDHDSIAVINIETALCCGIVEGHLEGNRMVNESTIALJGL	60
QY	60	CTGVJLILLSCGSSHLJFSEDFEFLYLLPPIIFNNGFOVKKQFENVNMTIMLSCATG	119
Db	61	ITGCVJLLCTGVNSRILJSEDFEFLYLLPPIIFNNGFOVKKQFENVNMTIMLSCATG	120
QY	120	TLLSCSIISFCGAVKIFKHLIDJLDFDGYLAIGAFATDSVCTQYLVSODETPLYSLV	179
Db	121	TLLSFVJITFCGAMJLEFKLDJGPELEDOYLAIGAFATDSVCTQYLNODEAPLYSLV	180
QY	180	FGESEVNDATSVJFENJIOSFDMTSPQPKIGHITGNKFLTFLSPFLYGIGILCAYII	239
Db	181	FGESEVNDATSVJFENJIOSFDMTSPQPKIGHITGNKFLTFLSPFLYGIGILCAYII	240
QY	240	KKLYFGHSTDRVJALMLMSJYLSJIAELFYLSGJLTVFECGIWMSHYTMHWNTSSRY	299

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Db 241 KICCFARHSTREVAIMILMAYLSYMLSHMLDLSGLITVFCGIVASHYTHWNTSSRV 300
QY 300 TTRHSPATLSFAETFFLYVGMADLIDIEKMFVKNSSQGLSVAVSSILVGLLVGRAFV 359
Db 301 TTRHSPATLSFAETFFLYVGMADLIDIEKMFVKNSSQGLSVAVSSILVGLLVGRAFV 360
QY 360 FPLSFLSNLAKKNSSDKISFRQOIIITWAGLMGAVSIALAYNKFTSGHSLHENAAMI 419
Db 361 FPLSFLSNLAKKNSHSPKISFNQOVIITWAGLMGAVSIALAYNKFTSGHSLHENAAMI 420
QY 420 TSTVTVVLFSTVVEGMLTKPLINLLPHKQMPGSHSSMTTSSPPKHETVPLDNDOP 479
Db 421 TSTVTVVLFSTVVEGMLTKPLINLLPHKQMPGSHSSMTTSSPPKHETVPLDNDOP 471
QY 480 SESDMITGPVAPPTALMLLRTPTHTVHKYRKFPDSEFMRPVYGGRGVFPVAPVQ 539
Db 472 --SDFVVG--OLTPQTNLOYLLTMTPTSRVHVRKFKDDKMRPMFGKGFVFPVGPSPIER 528
QY 540 S 540
Db 529 S 529

RESULT 14
ID 093YH2 PRELIMINARY: PRT: 534 AA.
AC 093YH2;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DE NA+/H+ ANTIporter, ISOFORM 1.
GN NHX1.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081.
RN [1]
RP SEQUENCE FROM N.A.
RA Venema K., Belyer A., Donaire J.;
RT "Cloning and characterization of two Na+/H+ antiporter isoforms from
   tomato."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ306630; CA084522.1; -.
SQ SEQUENCE 534 AA; 59037 MW; E4EF36FA4A0C0791 CRC64;

Query Match 65.7%; Score 1819.5; DB 10; Length 534;
Best Local Similarity 68.6%; Pred. No. 2.8e-131;
Matches 356; Conservative 66; Mismatches 88; Indels 9; Gaps 3;

QY 12 SDLETSDBASVSNLTFVALLCACIVLGHLEENRWNESTALILGLCTGVLLLSGG 71
Db 12 SILSDGQDVSDSTLTFALLCGCTIVLGHLEESRWINDSTLTVLGLSTGILLTKG 71
QY 72 KSHSLVFSSEDLFFLYLPLPIFNAGQVKKKQFFVFMFTIMLFGAIGTLISCSISFGA 131
Db 72 KSHSLHEDQGLFFLYVLPPIIFNAGQVKKKQFFRNVTIMLFGAIGTLISCSISFGA 131
QY 132 VKIRKHLIDFLDGDYLAIGAIPTAADSVCCTLOVLSODEPPLIXSLVFGGVNDATSV 191
Db 132 KELLGKIDIGFLERDYLAIGAIPTAADSVCCTLOVLSODEPPLIXSLVFGGVNDATSV 191
QY 192 VLFNATIGFDMTSPDPKIGLHFIIGNFLYFLSFTFLGAGIGLCAVYIIKKLYFRHSHTDR 251
Db 192 VLFNATIGFDMTSPDPKIGLHFIIGNFLYFLSFTFLGAGIGLCAVYIIKKLYFRHSHTDR 251
QY 252 EVALMMLSYLSYIMAEFLYLSGILVFFCGIVASHYTHWNTSSRVYTRHSPATLSFV 311
Db 252 EVALMMLSYLSYIMAEFLYLSGILVFFCGIVASHYTHWNTSSRVYTRHSPATLSFV 311
QY 312 AETPFFLYVGMADLIDIEKMFVKNSSQGLSVAVSSILVGLLVGRAFVFPPLSFLSNLAKK 371
Db 312 AETPFFLYVGMADLIDIEKMFVKNSSQGLSVAVSSILVGLLVGRAFVFPPLSFLSNLAKK 371
QY 371 AETPFFLYVGMADLIDIEKMFVKNSSQGLSVAVSSILVGLLVGRAFVFPPLSFLSNLAKK 371

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QY 372 NSDKISFRQOIIITWAGLMGAVSIALAYNKFTSGHSLHENAAMITSTVTVLFSTV 431
Db 372 NSDKISFRQOIIITWAGLMGAVSIALAYNKFTSGHSLHENAAMITSTVTVLFSTV 431
QY 432 VGLMKTPLINLLPHKQMPGSHSSMTTSSPPKHETVPLDNDOPDESMDITGPEVA 491
Db 432 VGLMKTPLINLLPHKQMPGSHSSMTTSSPPKHETVPLDNDOPDESMDITGPEVA 491
QY 492 RPTALMLLRTPTHTVHKYRKFPDSEFMRPVYGGRGVFPVAPVQ 530
Db 492 RPTALMLLRTPTHTVHKYRKFPDSEFMRPVYGGRGVFPVAPVQ 530
QY 483 RPSGLSILKEPSYTIHNMWRFDAPMRPLFGKGFV 521
Db 483 RPSGLSILKEPSYTIHNMWRFDAPMRPLFGKGFV 521

RESULT 15
ID 004655 PRELIMINARY: PRT: 457 AA.
AC 004655;
DT 01-JUL-1997 (TREMblrel. 04, Created)
DT 01-JUL-1997 (TREMblrel. 04, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE A_TM021B04.4 PROTEIN.
GN A_TM021B04.4.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=CV. COLUMBIA;
RC Dante M., Wamsley P., Gibson A.;
RT "The sequence of A. thaliana TM021B04."
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=CV. COLUMBIA;
RC Wash-U;
RT "The A. thaliana Genome Sequencing Project."
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA STRAIN=CV. COLUMBIA;
RC Waterston R.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF007271; AAB61069.1; -.
DR InterPro: IPR001179; FKBP_PPIase.
DR InterPro: IPR000676; Na_H_Exchange; 1.
DR Pfam: PF00999; Na_H_Exchange; 1.
DR PROSITE: PS00453; FKBP_PPIase; 1; UNKNOWN; 1.
SQ SEQUENCE 457 AA; 50611 MW; 0AF2F235F1A258EE CRC64;

Query Match 62.6%; Score 1732.5; DB 10; Length 457;
Best Local Similarity 75.4%; Pred. No. 1.1e-124;
Matches 341; Conservative 44; Mismatches 46; Indels 21; Gaps 3;

QY 5 ISSLLON--SDLETSDBASVSNLTFVALLCACIVLGHLEENRWNESTALILGLCTGV 63
Db 5 ISSLLON--SDLETSDBASVSNLTFVALLCACIVLGHLEENRWNESTALILGLCTGV 61
QY 64 VILLSGKSSHLVSEDLFFLYLPLPIFNAGQVKKKQFFVFMFTIMLFGAIGTLIS 123
Db 64 VILLSGKSSHLVSEDLFFLYLPLPIFNAGQVKKKQFFRNVTIMLFGAIGTLIS 121
QY 124 CSTIISGAVKIFKHLIDFLDGDYLAIGAIPTAADSVCCTLOVLSODEPPLIXSLVFGG 183
Db 124 CSTIISGAVKIFKHLIDFLDGDYLAIGAIPTAADSVCCTLOVLSODEPPLIXSLVFGG 181
QY 184 VVNDATSVVLFNATIGFDMTSPDPKIGLHFIIGNFLYFLSFTFLGAGIGLCAVYIIKKLY 231
Db 184 VVNDATSVVLFNATIGFDMTSPDPKIGLHFIIGNFLYFLSFTFLGAGIGLCAVYIIKKLY 231
QY 232 GLLCAVYIIKKLYG-----RHSTDEVALMMLSYLSYIMAEFLYLSGILVFFCGI 283
Db 232 GLLCAVYIIKKLYG-----RHSTDEVALMMLSYLSYIMAEFLYLSGILVFFCGI 283

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Db 242 GLISAAYVIRKLLYFGRWPHINCHRHSTDRBVALMMLMAYLSYMLAELFDLSGILTVFFCGI 301
QY 284 VMSHYTMHNVTSSRVTTBRHSFATLSFVAEPEIFLYGMDALDIEKKKFKVNSOGLSVAY 343
Db 302 VMSHYTMHNVTSSRVTTBRHSFATLSFVAEPEIFLYGMDALDIDKMRVSDPPTSIAY 361
QY 344 SSILVGLILVGRAAFVPEPLSFLSNLAKKNSDKISFRQIITIMWAGLMRGAVSIALAYNK 403
Db 362 SSILMGLVMVGRAAFVPEPLSFLSNLAKKNOSEKINFNMQYIMWSGLMRGAVSMALAYNK 421
QY 404 FTSGHTSLHENAIMITSTVTVVLFSTVVFGL 435
Db 422 FTBAGHTDVRGNALMITSTIVCLFSTVVRNL 453

Search completed: October 18, 2002, 12:26:45
Job time : 34 secs

